M33388 Human CYPCD AL366496 Human DNA AL366496 Human DNA D59962 Human Cosmi AC010222 Homo sapi AC010222 Homo sapi AL356748 Human DNA AC011669 Homo sapi AL33461 Human DNA AC012669 Homo sapi AC00364 Homo sapi AC00364 Homo sapi AC036773 Homo sapi AC036773 Homo sapi AC036774 Homo sapi AC013476 Homo sapi

97559 97860 101076

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148043

AX394457 Sequence AX394456 Sequence

AX207224 AX394457 AX394456 HUMCYP2D6 HSCYP2D7B AL365496

AX207224 Sequence AX394457 Sequence

Description

DB

Length

SUMMARIES

Human DNA
Homo sap1

AC013476 AC008541 AC011320 AC011120 AC068746 AC024920 AC024920 AC01866 AC01866 AC01866 AC01866 AC01866 AC01866 AC01866 AC01866 AC01866 AC01866

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Homo sapi Homo sapi sapi sapi Sequence

AL365497 H AC107016 H AP002768 H AC013829 H

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synthetic construct.

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artificial sequences.

( pases 1 to 1669)

Raimundo, S. and Zanger, U.

Polymorphisms in the human cyp2d6 gene promoter region and their use in diagnostic and therapeutic applications
Patent: WO 0155432-A 1 02-AUG-2001;
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0216538-A 2 07-MAR-2002;
Gemini Genomics PLC (GB)
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/db_xref="taxon:32630"
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Detection of cyp2d6 polymorphisms
Patent: WO 0218638-A 1 07-MAR-2002;
Gemini Genomics PLC (GB)
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Epidauros Biotechnologie AG (DE)
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/db_xref="G1:18130
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4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5836)
/gene="CYP2D6"
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Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
M33388
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Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4-hydroxylase (CYPED) Locus: sequence and identification of the polymorphic CYPED6 gene, a related gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Draft entry and computer-readable sequence for [Am. J. Hum. Genet. 45, 889-904 (1989)] kindly submitted by S.Kimura, 29-MAR-1990.

Location/Qualifiers
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4060. 4236,4427. 4568,4776. 4963,5418. 5559,5658.
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                                                                                                                ;
0
Score 50.6; DB 6;
Pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Am. J. Húm. Genet. 45 (6), 889-904 (1989)
90072069
2574001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome P450; cytochrome P450 IID6.
Human DNA, clone lambda2D-18/2.
Homo sapiens
                                                                                                          1; Mismatches
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4031 . 4207,4400 . 4540,4735 . 4922,5377 . 5518,5617 . 5868)
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4031 . 4207,4400 . 4540,4735 . 4922,5377 . 5518,5617 . 5795)
                                                                         Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostoml; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 13677)

3S Heim, M. H.

Direct Submission

AL Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND

3E (bases 1 to 13677)

3E Heim, M.H. and Meyer, U.A.

Evolution of a highly polymorphic human cytochrome P450 gene Cluster: CYP2D6

3D Genomics 14 (1), 49-58 (1992)

3D 1358797.
                        X58468.1 GI:30337
CYP2D7BP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                     See X58467, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
1. .13677
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Human CYP2D7BP pseudogene for cytochrome P450 2D6
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 DEFINITION
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            1675. 3224

Gene="CYP2D6"

Anote="G00-132-127; does not fit consensus"
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/number 2
2675. .322
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5658. .590
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HSCYP2D7B
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The true
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           RP11-449J3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kucherlapati,R., Montgomery,K., Renault,B., Yoon,S.J., Marynen,P.,
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AL589983(RP11-218H5). Assembly confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 38740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-JUN-1996) Department of Molecular Genetics, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY
                                                                                                   This sequence is the entire insert of clone RPI1-449J3 The true left end of clone RPI1-13G8 is at 158256 in this sequence. The tright end of clone RPI1-218H5 is at 89484 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from uni-directional dGTP big dye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 173728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="12p12-13; centromeric to ETV6" /clone="cosmid LL12NC01-N-136B11"
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Pred. No. 3.2e-05;
0; Mismatches 4;
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a 30718 c 30692 g 56095 t
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complement(5961, .6227)
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complement(5530, 5814/rpt for
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complement(683. .805)
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                                                                                                                                                                                                                                                                                                                                                                                                                           .131041
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nilarity 92.2%;
Conservative
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Kucherlapati, R.
Direct Submission
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Best Local Similarity
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 173728)

Arifiths, C.

Direct Submission

Al Submitted (01-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, humquery@anger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 30, 2001 this sequence version replaced gi:16973865.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNEEP: Information on the WORNEEP thter.//www.sanger.ac.uk/Projecte/Claimer.
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Human DNA sequence from clone RPI1-449J3 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.2%; Score 50.6; DB 9; 98.0%; Pred. No. 3.4e-07; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2729 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4107 g
                                                                                                                                                                                                                                                                                                                                                                                     /number=9
8267. .8306
/note="ACCCTTCCCC"
4541. .4734
/gene="CYP2D7BP"
                                                                  4735. .4922
/gene="CYP2D7BP"
                                                                                                                                                                                                                                                                      5519. .5616
/gene="CYP2D7BP"
                                                                                                                                                                                                      5377. .5518
/gene="CYP2D7BP"
                                                                                                                                    4923. .5376
/gene="CYP2D7BP"
                                                                                                                                                                                                                                                                                                                                           5617. .5868
/gene="CYP2D7BP"
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AL365496
AL365496.15 GI:17221187
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                                            /number=6
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Best Local Similarity 98.0°
Matches 50; Conservative
                                                                                                                                                                                                                                                     /number=8
                                                                                                                                                                                                                                                                                                                        'number=8
                                                                                                               'number=7
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AL365496
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86424 bp DNA 11near HTG 18-JUL-2000
5 5 clone CTC-265B3, WORKING DRAFT SEQUENCE,
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Mon May 6, 2000 this sequence version replaced g1:7239444.
                                                                                                                                                                                                                                                                                                                 Consensus quality: 56011 bases at least Q40
Consensus quality: 64421 bases at least Q30
Consensus quality: 66686 bases at least Q30
Consensus quality: 66686 bases at least Q20
Estimated insert size: 70000; pulse field gel estimation
Estimated insert size: 68835; sum-of-contigs estimation
Quality coverage: 3.97 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * 18 believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 2504 2603; contig of 2503 bp in length 2604 16029; contig of 13426 bp in length 16130 23795; contig of 666 bp in length 16130 23795; contig of 1665 bp in length 23795; contig of 1665 bp in length 32870 43827; contig of 10858 bp in length 43828 43927; gap of unknown length 43928 47285; contig of 10858 bp in length 43928 47285; contig of 13358 bp in length 47286 47385; contig of 13358 bp in length 47386 47385; contig of 1358 bp in length 47386 47385; contig of 13585 bp in length 47385; contig of 13585 bp in length 47385; contig of 13585 bp in length 47386 47385; contig of 13585 bp in length 47385; contig of 13585 bp in length 47385; contig of 13585 bp in length 47385; contig of 13586 bp in length 47386 47385; contig of 13585 bp in length 47385; contig of 135
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16 67913: contig of 16718 bp in length

17 68013: gap of unknown length

18 69185: contig of 1172 bp in length.

19 Location/Qualifiers
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21070 a 12867 c 11934 g 22513 t 801 other
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                                                                                                                                                                                                              Center Project Name: 380697, H426
Center clone name: CIT-HSPC_509C13
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/db_xrefr"taxon:9606"
                                                                                                                                      Web site: http://www.jgi.doe.gov
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8 ordered pieces.
AC10222.
HTG: HTGS_PHASE2; HTGS_DRAFT.
Homo sapiens.
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                                                                                                                                                                                           Project Information
                                                                                                                                                                                                                                                                                                Summary Statistics
                                                                                                           Center Code: JGI
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AC010222
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                              COMMENT
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Homo saplens chromosome 5 clone CTC-509Cl3, WORKING DRAFT SEQUENCE, AC022117
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                         /rpt_family="MER1"
complement(11157. .11388)
/rpt_family="MER1"
.11378. .11614
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                                                                                                                                                                                                                                                             /rpt_family="ALU"
complement(14487. 14781)
/rpt_family="ALU"
complement(15614. 15893)
/rpt_family="ALU"
complement(16162. 16280)
/rpt_family="MST"
                                                                                                                                                                                /standard_name="AFM211wb6"
/note="D12S98"
13016, 13298
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(17272. .17646)
/rpt_family="MER42"
complement(19390. .20690)
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complement(31600. 31987)
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complement(32098. .32504)
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                           /rpt_family="THE1b"
complement(11057...
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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complement(27323.
/rpt_family="ALU"
27765. .28012
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2 (bases 1 to 69185)
DOE Joint Genome Institute.
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37299. 37709
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DOE Joint Genome Institute.
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25798. .26082
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complement(34329.
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7940 c
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Homo sapiens
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Best Local Similarity
Matches 46; Conserva
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AC022117
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             RESULT 10
AL356748
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                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 81824 bases at least 040
Consensus quality: 81810 bases at least 030
Consensus quality: 85101 bases at least 030
Consensus quality: 85101 bases at least 030
Consensus quality: 85549 bases at least 020
Estimated insert size: 85000; pulse field gel estimation
Quality coverage: 8.75 in 020 bases; pulse field gel estimation
Quality coverage: 8.64 in 020 bases; pulse field gel estimation
04011ty coverage: 8.64 in 020 bases; sun-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
This sequence will be replaced
by the submittor.
This sequence will be preserved.

* by the finished sequence as soon as it is available and
the accession number will be preserved.

* 11209 11308: contig of 11208 bp in length

* 11200 11308: gap of unknown length
                                                                                                                                                 2 (bases 1 to 86424)
DDE Joint Genome Institute.
DIRECT Submission
Submitted (15.5EP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7710836.
Center: Joint Genome Institute
Center Code: JGI
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8: gap of unknown length length
8: gap of unknown length length
8: gap of unknown length
6: contig of 26968 bp in length
6: contig of 26968 bp in length
7: gap of unknown length
8: gap of unknown length
8: gap of unknown length
9: contig of 4457 bp in length
9: gap of unknown length
9: contig of 3716 bp in length
9: contig of 7075 bp in length
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1; Mismatches
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Center clone name: CIT-HSPC_265B3
                                                                                                         Sequencing of Human Chromosome 5
Unpublished
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                  DOE Joint Genome Institute
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                                                              (bases 1 to 86424)
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DD 50454 TCAAGACCAGCCTGGACAACATGTAAAACCCGGTCTCTACAAAAAATACA 50504

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Abbuilted (03-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, Call 13A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestEs clonerequest@sanger.ac.uk clone requestEs: clonerequest@sanger.ac.uk Clone on Dec 5, 2000 this sequence version replaced gi:11493283. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with that a sequence has been finished according to sequence submission orresponding to the overlapping clone, as we submit sequences with all overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria and follows. An attempt is made to resolve all sequence is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SMISSEROR: Tr: TREMBL: Wp:, WORMPEP: Information on the WORMPEP database can be found at database can be found at callows. Control or the WORMPEP database can be found at the constructed by the sanger centre chromosome 1 constructed by the Sanger Centre Chromosome 1 metry.//www.sanger.ac.uk/FROPChr1

RR4-686J16 is from the library RC1-4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/pacpac/home.htm

VECTOR: DOTGY: DOTGY-CONE SAUGHT of Conservation only once, except for a 100 base overlap. The true left end of clone RP4-686J16 is at 1573 in this sequence. The Location that the database sections only once concept of all one RP4-866J16 is at 1573 in this sequence.
AL356748 97559 bp DNA linear PRI 04-DEC-2000 Human DNA sequence from clone RP4-686J16 on chromosome 1, complete sequence.
                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2008. .2639
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/note="AluSx repeat: matches 1.
1512. .1812
/note="AluSx repeat: matches 1.
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/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPCI-4"
                                                                                                                              AL356748
AL356748.20 GI:11558567
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Laird, G.
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7399. 34281
73999. 34281
700te="Alux repeat: matches 17. 311 of consensus"
74351. 34640
700te="Alux repeat: matches 1. 287 of consensus"
74351. 34640
7577. 36047
700te="Alux repeat: matches 1. 313 of consensus"
7737. 37627
700te="Thus repeat: matches 1. 313 of consensus"
77057. 38173
700te="FLAM_C repeat: matches 1. 118 of consensus"
78057. 38173
700te="FLAM_C repeat: matches 1. 118 of consensus"
78191. 38190
700te="Charlled repeat: matches 1855. 1871 of consensus"
78191. 38449
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20111. 22/041

27111. 27147

/note="Mill pepat: matches 110. .180 of consensus"
27111. 27147

/note="match: Gas: Em:AQ136115"

27131. .27224

27131. .27224

27132. .27234

27139. .27631

/note="match: GSS: Em:AQ556313"

/note="match: GSS: Em:AQ58882"

/note="match: GSS: Em:AQ798882"

/note="match: GSS: Em:AQ438628"

/note="match: GSS: Em:AQ438628"

/note="match: GSS: Em:AQ436115"

/note="match: GSS: Em:AQ436115"

/note="match: GSS: Em:AQ436115"

/note="match: GSS: Em:AQ436115"

/note="match: GSS: Em:AQ436128"

/note="liz repeat: matches 2587. .2699 of consensus"
29562. .29638

/note="liz repeat: matches 2660. .2705 of consensus"
                                            of consensus"
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                                                                                  /note="MIR repeat: matches 80. .233 of consensus" 25186. .25354 //note="MIR repeat: matches 77. .262 of consensus" 25530. .25827 //note="MIR repeat: matches 1. .298 of consensus" complement(26592. .27148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Alusx repeat: matches 1, .302 of consensus" 38450, .38544
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                                          repeat: matches 5528.
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ilarity 90.2%; Pred. No. 4.5e-05;
Conservative 1; Mismatches 4;
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complement(26720. .27017)
/note="match: GSS: Em:AQ100816"
complement(26833. .27131)
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/note="match: GSS: Em:AQ532789"
/note="match: GSS: Em:AQ532789"
/note="match:
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26971. .27041
                                     /note="L1ME1 r
23288. .23435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thote="Alusq repeat: matches 37. .311 of consensus" 18470. .18669 force="LIMC/D repeat: matches 5423. .5612 of consensus" 8751. .18902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ### Annual Property in the Property of Consensus ### Anote="L2 repeat: matches 2691. 2749 of consensus ### Anote="L2 repeat: matches 2691. 2749 of consensus ### Anote="L2 repeat: matches 2217. 2298 of consensus ### Anote="Alux repeat: matches 1. 305 of consensus ### Anote="Alux repeat: matches 1. 305 of consensus ### Anote="L2 repeat: matches 2023. 2217 of consensus complement(10541. 11084)

### Anote="In Table 10541. 11084]

### Anote="Match: GSS: Em:A0316052"

### Anote="Match: GSS: Em:A0316052"

### Anote="Match: GSS: Em:A2121092"

### Anote="Match: GSS: Em:A2121092"
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18928. .19233
                                                                                                                                                                                                                                                      19692. .19772
/note="%luJ/FLAM repeat: matches 5. .85 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note~"MER45B repeat: matches 437. .492 of consensus"
1/344. .17892
//note~"match: GSS: Em:B50102"
17496. .17773
                                                                                                                                    2676. .2813
/note="MLT1F repeat: matches 401. .534 of consensus"
complement(2908. .3284)
                                                                                                             .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LTR9B repeat: matches 445. .560 of consensus"
12397. .12857
conplement(13076. .13897)
complement(13076. .13897)
                        /note-...MLT1H repeat: matches 51. .130 of consensus."
7477. .255
/note--MLT1H repeat: matches 202. .288 of consensus."
2676. .2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13492. .13591
/note="L2 repeat: matches 2388. .2487 of consensus"
13685. .13725
                                                                                                                                                                                                                           1270. 3365
/note="L2 repeat: matches 2075. .2178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2709. .2749 of consensus" (4198. .14273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 2584. .2708 of consensus"
6477. .16612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1073. .8228
'note="MIR repeat: matches 106. .245 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"AluSx repeat: matches 5. .312 of consensus"
/note="MIR repeat: matches 78, .252 of consensus"
2328. .2414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"MIR repeat: matches 85. .228 of consensus"
complement(16832. .17296)
/note-"match: GSS: Em:AQ700892"
17109. .17167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20881, .20991
/note="MIR repeat: matches 16. .142 of consensus"
21460. .21617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 20. .184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9235. .19296
"note="31 copies 2 mer aa 74% conserved"
19553. .19654
                                                                                                                                                                                                                                                                                                      7092. 7341
/note="match: STS: Em:G15587"
complement(7568. .8088)
/note="match: GSS: Em:AQ707880"
complement(7909. .8281)
/note="match: GSS: Em:AQ35467"
8073. .8228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'noted"L2 repeat: matches 2673.
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note="match: STS: Em:G18185"
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RAMIMELLAS EUCHDETIS; FILMATES; CATALTHII; HOMINIDAGE; HOMO.

RAMIDYD, D.M., Adams, C., Adio-Odulola, B., All-coman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Area, J.R., Ayele, M., Banks, T., Barboria, J. Benton, J., Binder, C., Area, J.R., Ayele, M., Banks, T., Boudek, J., Benton, J., Burket, C., Burnell, K. L., Byrd, N. C., Chreez, J., Chen, R., Chon, Z., Chiu, D., Chowalty, I., Christopoulos, C., Chen, G., Chen, R., Chola, D., Chowalty, I., Christopoulos, C., Chen, G., Cox, C., Denn, A.L., Dind, M. C., David, R., Delado, C., Denn, A.L., Dind, Y. Dinh, H. H., Delaney, K. M., Delgado, C., Denn, A.L., Ding, Y. Dinh, H. H., Delaney, K. W., Delgado, C., Denn, A., Chowalty, I., Christopoulos, C. Chentrattic, D., Cox, C., Coyle, M., Dugan-Footh, S. Purbin, H. M., Delaney, K. W., Delgado, C., Denn, A., Gardis, A., Garner, T., Garza, N., Hanlton, K. J., Earnhart, C., Edgar D., Edwards, C.C., Elhaj, C., Emerling, S., Enratz, P. Gabisi, A., Gardis, A., Garner, T., Garza, N., Hamilton, K. Han, J., Harris, C., Liu, J., Liu, M., Loulseged, H., Lozado, R. Jia, Y. Hulyk, S., Hume, J., Holloway, C., Hollies, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Johnson, R., Joliver, S., Joudah, S., Karlsson, E., Kelly, S., Marcher, S., Hond, C., Liu, J., Liu, M., Loulseged, H., Lozado, R. Jia, Y. Lu, X., Lucier, M., Miller, R., Martinez, E., Maschmari, M., Mapue, P., Marniney, E., McLeod, M.P., Martinez, E., Masce, M., Ballon, D., Wortan, M., Maller, M., Montgomery, R., Mortgan, M., Martinez, S., Moscer, M., Miller, M., Montgomery, R., Tanerisa, K., Sterer, S., Socett, G., Sher, H., Shan, C., Shockher, S., Warde, M., Tanerisa, K., Tanerisa, K., Sterer, S., Soch, C., Shan, H., Shan, M., Syatek, M., Tabor, P., Tanerisa, A., Tanerisa, M., Syatek, M., Tabor, P., Tanerisa
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Direct Submission
Submitsed (09-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 97860)
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Submitted (01-MAR-2002) Human Genome Sequencing Center, Department Submitted (01-MAR-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 97860)
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Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
On Mar 1, 2002 this sequence version replaced gi:15625994.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        Homo sapiens
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                                                                    ORGANISM
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/rpt_family="MIR"
(239. .6325
/rpt_family="LIR"
/rpt_family="L2"
   repeat_region
                                        repeat_region
                                          CLONE LENGTH: This sequence does not necessarily represent the
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar. QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. /note="overlaps bases 1. .208 of clone AC007537" /function="clone overlap" 1. .144 /rpt_family="Tigger3(Golem)" /organism="Homo sapiens" /db_xref="taxon:9606" /rpt_family="MIR" /rpt_family="Limec" complement///or complement(1586, 1995) /rpt_family="MSTA" complement[4287. .4578)
/rpt_family="AluSx"
complement(4579. .5154)
/rpt_family="LIMEc" /rpt_family="AluJo" complement'fers .2884) complement (3260. 3410) /rpt_family="Limec" complement (5458. .5880) /rpt_family="LIMEc" complement(245.7552) /rpt_family="AluJb" Location/Qualifiers /clone="RP11-52513" complement(1. .208) /rpt_family="Alusg" /rpt_family="L2" complement(2584. /rpt_family="L2" /chromosome="] .97860 QUALSTAT-REPORT, 2041 repeat_region misc_feature source FEATURES

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Submitted (07-AUG-1996) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone IMPORTANT: This sequence is the entire insert of clone 37M17. The true left end of clone 37M17 is at 1 in this sequence. The true right end of clone 37M17 is at 10006.

37M17 is from the human PAC library.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .165 of consensus
                                                                                                                                                                                                                                                                                    /note-"Alu repeat: matches 289. .1 of consensus" 2344. .2515
/note-"MER20 element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Alu repeat: matches 297. .1 of consensus"
21383. .21449
21046. .1 element fragment"
21494. .21696
/note="L1 element fragment"
21751. .22083
/note="L1 element fragment"
22141. .22282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note" "Alu repeat: matches 308. .1 of consensus"
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                                                                                                                                                                                                                                                                                                                               conserved"
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19845. 19919
/note="MERIA element fragment"
20108. 20175
/note="17 copies of 4 mer 91 % conserved"
20205. 20485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14836. 14893

/note="MERSA element fragment"

15443. 15796

/note="2 copies of 177 mer 98 % cc

15860. 16159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /hote="Alu repeat: matches 308.
16169. 16267
/hote="MIR element fragment"
17729. 18030
/partial
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18690. 19019
Note "MSTA element fragment"
19564. 19919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Alu repeat: matches 308.
2288: .2238: .22356
/note="L1 element fragment"
22356: .22496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"MSTA element fragment" 22907. .23005
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note-"L1 element fragment"
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22892. .23000
                                                                                                                                    1. .101076
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/db_xrefo"taxon:9606"
/chromosome:"X"
                                                                                                                                                                                                                     /clone="RP1-37M17"
/clone_lib="RPC1-1"
3. .281
/partial
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mistry, S.
Direct Submission
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Human DNA sequence from PAC 37M17 chromosome X.
278022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MER5B"
23896. .240^1
                                                                                                                                                                                                                                                                                                                       complement(16048. 16345)
/rpt_family="AluJo"
16464. 16613
                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
complement(19179. .19306)
/rpt_family="MER81"
19880. .19931
                                                                                                                                                                                                                                                                complement(13122. .13324)
/rpt_family="MER63A"
14663. .14940
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complement(20883. .20941)
/rpt_family="MIR"
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complement(21358. .21432)
/rpt_family="MER5B"
complement(22435. .22532)
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complement(25359. .25724)
/rpt_family="L2"
26400. .26684
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(0502, 1062,
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3646. RAGA
                                                                    complement(8693. .8965)
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                                                 /rpt_family."AT_rich"
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24042. .24355
                                                                                                                                                                                                                 rpt_family~"(TTG)n"
1416. .11591
rpt_family~"FRAM"
                                                                                                                                                                                                                                                                                                                   'rpt_family="MER58B"
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.9019. .19116
                                                                                                                                                                                    rpt_family~"AluJo"
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                                                                                                                                                   /rpt_familý~"MIR"
10900. .11232
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|7260. .17568
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/note="Alu repeat: matches 308. .1 of consensus" 2927. .30033
/note="MLTA element fragment" 2943. .30005
/note="MSTC element fragment" 30722
/note="All repeat: matches 1. .308 of consensus" 32718. .32789
/note="MSTA element fragment" 32784 / 32896
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52994. .53107
'Partial
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                                                                                                                       /note="Li element fragment"
24136. .24249
/note="Li element fragment"
24312. .25277
/note="Li element fragment"
26752. .27026
/note="MER42A element fragment"
26776. .26875
/note="Li element fragment"
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Anote="THELB element fragment"

32923. .33068

Anote="NGTA element fragment"

32961. .33043

Anote="THELB element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35360. 41487

Anote="Li element fragment"

41609. 41727

Anote="MLTID element fragment"

A1134. 42220

Anote="MLTIE element fragment"

42604. 44783
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18908. .49199
/note="MSTC element fragment"
22918. .23211
/note="THELB element fragment"
23079. .23258
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46842. .47139
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29106. .29376
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45595, .45894
/partial
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53138. .53218
                                             23079. .23258
/note="MSTA element fragment"
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1397, .51711
                                                                            23384. .23602
/note≈"L1 element fragment"
23772. .23957
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44819. .45081
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Homo sapiens chromosome , clone RP11-8L20, complete sequence.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boyuslawity, L., Boukhgalter, B., Brown, A., Castle, A., Calangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome, clone RP11-8L20
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90.2%; Pred. No. 4.5e-05;
tive 1; Mismatches 4;
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/note="MER1B element fragment"
59781. .60056
/note="L1 element fragment"
53226. .53363
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Submitted (Ja-ARR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

(bases 1 to 106314)

Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Chazaro,B., Chocpel,Y., Colangelo,M., Collins,S., Collins,S., Collins,S., Collins,S., Collins,S., Collins,S., Collins,S., Cook,A., Cook,A., Cook,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Gander,S., Gordette,M., Graham,L., Grand Plerree,N., Hagos,B., Horton,L., Hulme,W., Illev,I., Johnson,R., Jones,C., Kamat,A., Kartas,A., Kells,C., LaRocque,K., Landarses,R., Landers,T., Lehcczky,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., Macdonald,P., Major,J., Mayor,C., Nathens,L., Mihova,T., Mlenga,V., Murphy,T., Toylonell,P., O'Neil,D., O'Lonnell,P., O'Neil,D., O'Lonnell,P., O'Neil,D., Nette,St., Raymond,C., Rette,R., Phunkang,P., Pierre,N., Polara,V., Raymond,C., Rette,R., Phunkang,P., Pierre,N., Schauer,S., Schupback,R., Senaca,S., Severy,P., Spencer,B., Stange-Thoman,N., Stojanovic,N., Standan,S., Severy,P., Spencer,B., Stange-Thoman,N., Stojanovic,N., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Lainer, M., And Zody,M., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Direct Submission.
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Leuc, C., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKenran, K., McLaughlin, J., Moltrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Poterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

L. Submitted (17-NoV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research
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Contact: sequence_submissions@genome.wi.mit.edu
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Only the first 106.3 kilobases of this clone are being submitted. The remainder overlaps accession number AC016866 [WICGR project L3452].
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Project Information
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26
                                                                                                                                               /organism∵"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family:"L3"
                                                                                                                                                                                                                                                                    complement(365. .803)
/rpt_familyo"MER41A"
complement(2476. .2522)
/rpt_familyo"L2"
                                                                                                                                                                                                                                                                                                                                                                                         complement(3428. .3738)
/rpt_family~"Aluy"
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8571. .8882
/rpt_family-"AluY"
complement(9103. .9412)
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/rpt_family="L3"
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           Center project name: L1284
Center clone name: 8_L_20
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/rpt_familye"LIMB3"
4124. 4417
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                                                                                                                                                             /db_xref="taxon:9606"
/clone="RP11-8L20"
                                                                                                                                                                                                           complement(1. .60)
/rpt_family="MER41A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family~"AluSg"
5381. .5683
/rpt_family~"AluY"
5684. .5842
                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family~"L1MB3"
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/rpt_family~"MLT11"
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                                                                                                                                                                                                                                                      /rpt_family."Aluy"
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418. .4598
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876. .4967
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us-09-942-310-2_copy_5_5.rge

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30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; W., WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 10. constructed by the Sanger Centre Chromosome 10 Mapping Group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chr10 RPI1-359E7 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further dettails see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP11-359E7 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-359E7 is at 12428 in this sequence. The true right end of clone RP11-359E7 is at 2000 in this
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DOB Joint Genome Institute.
Direct Submission
Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (15-A0622001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (bases 1 to 130965)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 5 clone CTC-230L18, complete seguence.
ACO26773
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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Pred. No. 4.4e-05;
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24571 c 26217 g 36558
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/organism="Homo sapiens"
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humguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 17, 2001 this sequence version replaced gi:14970653.

During sequence assembly date is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL133461 124328 bp DNA linear PRI 16-NOV-2001
Human DNA sequence from clone RPI1-359E7 on chromosome 10, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 90.2%; Pred. No. 4.5e-05;
Conservative 1; Mismatches 4;
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/rpt_family="MLT1F1"
complement(11180. 11286)
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/rpt_family="AluSg1"
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/rpt_family="LiMC3"
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/rpt_family="MIR"
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DoE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
L Submitted (14-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
6 (bases 1 to 130965)
S DoE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
L Submitted (16-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 14, 2001 this sequence version replaced gi:15187257.
Location/Qualifiers
1. 130965
Contonesome="5"
//db_xrefe" taxon:9606"
//chromosome="5"
//clone="CTC-230118"
//clone="CTC-230118
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estinated Total Number of Errors is 0.3."
41144 a 24526 c 23780 g 41515 t
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Search completed: February 11, 2003, 05:28:18 Job time: 293.499 secs

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Human neuregulin-1 Human neuregulin-1

Human nervous syst Human cardiovascul

Human WKL-1 genomi Human osteoblast d

Scoring table:

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Minimum DB : Maximum DB :

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Human osteoblast d Genomic sequence #

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Human

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Cytochrome P450; CYP2D6; promoter; drug metabolism; diagnosis; therapy; ds.
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/note- "amplification primer upf14"
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/note- "sequencing primer F2"
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                                                          February 10, 2003, 20:43:59; Search time 20.723 Seconds (without alignments) 5542.256 Million cell updates/sec
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       GenCore version
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9432
401
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Match
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Human reproductive Human cDNA encodin

ovarian

Human Нишап CDNA encoding nove

human;

/*tag= e /note= "sequencing primer R3" complement (968..988)

primer_bind

Human cancer relat

Score

Result 80. 26459786

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602..620

primer_bind

2

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f "sequencing primer F3"

..1143

*tag=

g "sequencing primer R4"

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Sequence 1669 BP; 413 A; 376 C; 534 G; 338 T; 8 other;
        /note= "se
1605..1623
  /note=
1124..1
                                   WO200155432-A2
    primer_bind
          primer_bind
                primer_bind
                                       02-AUG-2001
                      5'UTR
                         CDS
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The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene. The promoter region was amplified by PCR from leucocyte DNA of over 50 individuals, and sequenced.

8 Previously unknown single nucleotide polymorphisms (SNP) were identified. These were at: base 36 (base -1584 according to the muman Cytochrome P450 Allele Nomenclature), where the SNP was C to G, occurring at an estimated frequency of approximately 20% in the whole population, and resulting in increased enzyme activity; consition 194 (-1426), C to T, approximately 20% frequency, neutral function; position 385 (-1235), A to G, approximately 50% interpretation 199 (-1426), C to T, approximately 50% frequency, neutral function; position 620 (-1000), G to A, approximately 30% frequency, unknown function; position 940 (-680), G to A, approximately 30% frequency, unknown function; position 950 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position 50 (-1000), G to A, approximately 30% frequency, unknown function; position is claimed (see Ani26179).

The invention provides a method of diagnomicing alsorder related to reduced or enhanced capacity for clearance of Cyp206 substrates

Contact A, approximately approximately for clearance of Cyp206 substrates

Contact A, by determining the presence of a mutation in the Cyp206

Contact A, by with increased environmentation in the Cyp206

Contact A, contact A, contact A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A polynucleotide capable of hybridizing to CYP2D6 promoter useful for the optimization of drug therapies using substrates of cytochrome P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolizers and therefore allow unantitative predictions to be made on in vivo drug metabolism capacity, thus providing a very potent tool for improving the therapy of diseases with drugs that are targets of the CYP2D6 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           correlation between genotype and phenotype in the CYP2D6 polymorphism. Testing for the mutation will allow the identification of intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1584 bp with increased enzyme activity significantly improves the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partial
/note= "5' region of CYP2D6 coding region"
                                                                                                                                                                                                             "amplification primer upr1669"
'*tag= h
'note= "sequencing primer R5"
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1620..1669
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                                                                                                                                                                                                             /note= "amp
1532..1619
                                                                                                   .1669
                                                                                                                                                                 *tag=
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A polynucleotide capable of hybridizing to CYP2D6 promoter useful for the optimization of drug therapies using substrates of cytochrome P-450
                                               Gaps
                                                                                                                                                                                                                                                                                 Human cytochrome P450 CYP2D6 gene promoter (G mutation at -1584 bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antagonist, tricyclic antidepressant, selective serotonin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP2D6 promoter. The novel variant forms of the CYP2D6 gene provided by the invention provide the potential for the development of a pharmacodynamic profile of farugs for a given patient. The finding and characterization of variations in the CYP2D6 gene, and diagnostic tests for the discrimination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene, which includes G at position 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature). The presence of C at position -1584 bp is a marker for low enzyme activity, whereas there is strong association of at position -1584 bp with increased enzyme activity. The C to G single nucleotide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates (antiarhythmic, beta adrenergic receptor
                                             0;
                Length 1669;
                                                                                         1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "5' region of CYP2D6 coding region"
                                             Indels
                                                                                                                                                                                                                                                                                                            Cytochrome P450; CYP2D6; promoter; drug metabolism; diagnosis; therapy; single nucleotide polymorphism;
             Score 50.6; DB 22;
Pred. No. 1.2e-09;
                                               ó
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers replace(36,G)
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99.2%; SCULL
100.0%; Pre
0; )
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                                                                                                                                                                                                                                                                                                                                                                                                                                     frequency= "20%"
532.1619
                                                                                                                                                                                       BP.
                                                                                                                                                                                   AAH26179 standard; DNA; 1669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
1620..1669
/*tag= c
                                                                                                                                                                                                                                                17-SEP-2001 (first entry)
        Query Match 99.2%
Eest Local Similarity 100.0
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                           Key
variation
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                                                                                                                                                        RESULT 2
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WO200218638-A2
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                                                                                                                                                                                                                                                                     Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
ligase-based sequenced determination; drug metabolism; chromosome 22;
gene; polymorphism; ds.
                                                                                                                Gaps
different alleles in human individuals, provide a very potent tool for improving the therapy of diseases with drugs that are targets of the CYP2D6 gene production, and whose metabolism is therefore dependent on CYP2D6 activity.

Note: The present sequence is not shown in the specification but is derived from the CYP2D6 promoter sequence given in the Sequence Listing (see AAH26169).
                                                                                                                                                                                                                                                       Human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New sequence determination oligonucleotides, useful for detecting
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0
                                                                                             Length 1669;
                                                                                                                                51
                                                                                                                                         1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA
                                                                                                              Indels
                                                                         Sequence 1669 BP; 413 A; 376 C; 535 G; 338 T; 7 other;
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                                                                                           DB 22;
                                                                                                    Pred. No. 1.2e-09;
1; Mismatches 0;
                                                                                            Score 50.6;
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"Polymorphic site"
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"Polymorphic site"
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"Polymorphic site"
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"Polymorphic site"
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"Polymorphic site"
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"Polymorphic site"
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                                                                                                                                                                                                                                                                                                                                cocation/Qualifiers
                                                                                                                                                                                                AAD34214 standard; DNA; 1680 BP
                                                                                          Query Match
Best Local Similarity 98.0%;
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note
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                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                 AAD34214;
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                                                                                                                                                                             RESULT 3
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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenoblotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, us hybridisation-based diagnostic assays, and as components of diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as
                                                                                                                                                                                                                                                                                                                                    microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
ligase-based sequenced determination; drug metabolism; chromosome 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New sequence determination oligonucleotides, useful for detectin polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50.6; DB 24; Length 1680; Pred. No. 1.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1680 BP; 413 A; 379 C; 539 G; 342 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     딦
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligase-based sequence determination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                  Claim 1; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD34213 standard; DNA; 9432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2001; 2001WO-IB01544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 51; Conservative
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above methods.

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This sequence represents a single nucleotide polymorphism (SNP) of the human neuregulin-1 associated gene 1 (NRG1AG1) of the invention. The NRG1AG1 gene is also referred to as the human Schizophrenia gene. The invention also relates to fragments or variants of the gene and the invention also relates to fragments or variants of the gene and the Convention also relates they encode. The NRG1AG1 nucleic acids and convention of the polypeptides may be used in the prevention, diagnosts and treatment of diseases associated with inappropriate NRG1AG1 expression. For example, they may be used to treat disorders associated with decreased expression the activity of NRG1AG1 by expressing inactive proteins or to supplement the patients own production of NRG1AG1. Additionally, the gene may be used to produce NRG1AG1 polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene may calso be used as DNA probes and primars in diagnostic assays to detect and therefore which patients may be in need of restorative therapy. The CNRG1AG1 polypeptides may also be used as antigens in the production of antibodies against NRG1AG1 and in assays to identify modulators of antibodies and activity. Anti-NRG1AG1 antibodies antagonists.
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hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for preventing diagnosing and treating schizophrenia -
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neuregulin gene single nucleotide polymorphism SNP8NRG1022025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; neuregulin-1 associated gene 1; NRG1AG1; Schizophrenia gene; gene therapy; single nucleotide polymorphism; SNP; ds.
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0
                                                                                                                                 Length 9432;
                                                                                                                                                                                                                         TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 51
                                                                                         Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 other;
                                                                                                                                                                        Indels
                                                                                                                                Score 50.6; DB 24;
Pred. No. 1.9e-09;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gulcher JR;
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llarity 98.0%;
Conservative 1
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ID AAK96153 standard; DNA; 401
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                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stefansson H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                           gene.
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                                                                                                                                                                  50;
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                                                                                                                                                                                                                                                                                                                                                                       AAK96153;
                                                                                                                                Query Match
Best Local
                                                       CYP2D6
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                RESULT 5
 22222x8
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The invention also relates to fragments or variants of the neuregulin I are invention also relates to fragments or variants of the neuregulin I and treatment of diseases associated with inappropriate neuregulin I expression, such as schizophrenia. For example they may be used to treat disorders associated with decreased neuregulin I expression by rectifying mutations or deletions in a patient's genome that affect the actifying neutations or deletions in a patient's genome that affect the actifying neutations or polypeptides. Additionally, the gene may be used to produce the neuregulin I protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar content in the manner of the content of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restorative therapy. The protein may also be used as antigens in the production of antibodies against neuregulin 1 and in assays to identify modulators of neuregulin 1 expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity.

The antibodies may also be used as diagnostic agents for detecting the
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neuregulin gene single nucleotide polymorphism SNP8NRG1022025.
                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a single nucleotide polymorphism (SNP)
                                                                                                                  Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuregulin 1 nucleic acids and proteins useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 401;
                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                     Human; neuregulin 1 gene; schizophrenia; gene therapy; SNP; single nucleotide polymorphism; ds.
                                                                                                                                                                        Indels
                                                                                                                                                                                                                     1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACA
                                                   Sequence 401 BP; 107 A; 88 C; 93 G; 112 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 401 BP; 107 A; 88 C; 93 G; 112 T; 1 other;
                                                                                           Score 42.6; DB 22;
Pred. No. 9.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gulcher JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42.6; DB 22
Pred. No. 9.4e-07;
                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing and treating schizophrenia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 246; 756pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence of neuregulin 1 in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steinthorsdottir V,
                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                            83.5%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.5%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2001; 2001WO-US06377.
                                                                                                                                                                                                                                                                                                                                                                                                               AAK97646 standard; DNA; 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DECO-) DECODE GENETICS EHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                  45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514841/56.
                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK97646;
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                           RESULT 6
AAK97646/C
                                                                                                                                                                  Matches
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1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACA
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                                                                                                               ABV52891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
 Gaps
                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                         1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 51
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 447 BP; 84 A; 132 C; 101 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #1803.
 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 1803; 103pp; English.
1;
                                                                                                                                                                       AAS65999 standard; cDNA; 447 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                  (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABG01812
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT,
45;
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                                                                                                                                                                                                             AAS65999;
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Matches
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    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogento potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid molecule (I) compa nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is affilicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 556 BP; 168 A; 119 C; 127 G; 141 T; 1 other;
                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 52882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 10252; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
                                                                                                                                                                      ABV52891 standard; cDNA; 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-183319P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate
pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a patient;
                                                                                                                                                                                                                                                                                         17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-2000;
16-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001.
                                                                                                                                                                                                                               ABV52891;
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patient;
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RESULT

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Gaps

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Indels

Length 447;

83.5%; Score 42.6; DB 23; 88.2%; Pred. No. 9.7e-07; iive 1; Mismatches 5;

Query Match 83.5 Best Local Similarity 88.2 Matches 45; Conservative

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20-FEB-2001; 2001WO-US05171
           WO200160860-A2
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0
                                                                                                                                                                                                                                                                                                                                                                                                      with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
                                                                                                                                                                                                                                                                                                                           New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                               cytostatic; gene expression; gene mapping; tissue profilling; erapy; cancer; tumour; gene; ss.
                                                                                                                                                                                                                                                                         Randazzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pot D, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3043; 883pp + Sequence Listing; English
                                                                                                                                                                                                                                                                         Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 565 BP; 185 A; 96 C; 117 G; 167 T; 0 other;
                                                                         Human cancer related polynucleotide SEQ ID NO 3043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.5%; Score 42.6; DB 24;
ilarity 88.2%; Pred. No. 1e-06;
Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                         Sudduth-Klinger J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate expression marker cDNA 50269
                                                                                                                                                                                                                                                                        Garcia PD, Sudduth-Klinger Scott EM, Zhang G, Kassam A,
                                                                                                          gene therapy; cancer; tumour; gene;
          ABN63076 standard; cDNA; 565 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV50278 standard; cDNA; 578
                                                                                                                                                                                              16-AUG-2001; 2001WO-US25840
                                                                                                                                                                                                                   16-AUG-2000; 2000US-226326P
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                        WPI; 2002-241905/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 45; Conserv
                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                   WO200214500-A2
                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy.
                                                                                                                                                                                                                                                                         Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                    28-JUN-2002
                                                                                                                                                                         21-FEB-2002
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                                                                                                                                                                                                                                                                                    Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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ABN63076
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.5%; Score 42.6; DB 23; Length 578; llarity 88.2%; Pred. No. 1e-06; Conservative 1; Mismatches 5; Indels 0
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                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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    The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, care archive (e.g. cancer), influentials, neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. athma), cardiovascular disorders (e.g. athma), cardiovascular disorders (e.g. athma), cardiovascular disorders (e.g. athma), reproductive disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infertious disorders (e.g. infertility) and infertious disorders (e.g. infertility) and infertion can also be used in gene therapy.

AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention can also be used in gene therapy.

ANGUE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPDO.
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                         Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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                                                                                                Disclosure; SEQ ID No 2276; 1180pp; English.
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2000US-0180628.
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WPI; 2001-465566/50
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24-FEB-2000;
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16-MAR-2000;
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isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atheroscierosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. inflammatory disorders inflammatory disorders (e.g. inflammatory disorders in
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Rosen CA, Barash SC, Ruben

WPI; 2001-451930/48.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system

Claim 1; SEQ ID No 1902; 674pp; English.

Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardior as nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal

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12-SEP-2000;
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14-SEP-2000;
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29-SEP-2000;
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27-SEP-2000;
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21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasctropic; dog; antirheumatic; antiprollferative; cytostatic; cardiant; neuroprotective; ophthalmological; valuedes; fungicide; cancer; ophthalmological; valuerary; gene therapy; autoimmune disease; neoplasm; hyperprollferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; breast; liver; cardiovascular disorder; ds; fungal infection; viral infection; ocular disorder; endocrine disorder; bound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                     Length 4962;
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                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                Query Match 83.5%; Score 42.6; DB 22; Best Local Similarity 88.2%; Pred. No. 1.9e-06; Matches 45; Conservative 1; Mismatches 5;
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2000US-0180628.
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2000US-0186350.
2000US-0189874.
2000US-0199123.
2000US-0205515.
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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14-JUL-2000;
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26-JUL-2000;
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200008-023537037
200008-0237037
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2000US-0231968.
2000US-0232397.
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Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigen polypeptides of the invention. Useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimens's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, as glomerulonephritis and respiratory disorders such as astmma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 1903; 674pp; English.
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                                                                                                                                                   2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0249214.
2000US-0249215.
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2000US-0249218.
2000US-0249248.
2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249267.
2000US-0249297.
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                                                             2000US-0246609
                                                                             2000US-0246610.
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                          08 - NOV - 2000;
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05-DEC-2000;
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(a) combining the PSA expressing cells with a candidate drug in the presence of an androgen for sufficient time for detectable expression of the gene, and (b) detecting the level of expression of the gene as compared to the level of expression in the absence of the candidate drug. The method can be used to evaluate the potential of a
 specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                      Promoter; enhancer; 5' non-coding region; hKLK2; kallikrein; hGK-1; PSA; prostate specific antigen; prostate cancer; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening drugs for treatment of prostate cancer - uses prostate specific antigen expressing cells
                                                                                            0;
                                                              Length 4962;
                                                                                                                                       2690 TCAAGACCAGCCTGGACAACATGGTGAAAACCCTGTCTCTACAAAAAATACA 2740
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                                                   Score 42.6; DB 22;
Pred. No. 1.9e-06;
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/note= "enhancer active fragment"
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/note= "promoter active fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                AAV17618 standard; DNA; 12047 BP
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88.2%;
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96US-0692759.
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                                                                                            45; Conservative
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specification, but
                                                                            Best Local Similarity
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CC compound as a therapeutic agent for the treatment of prostate
CC cancer. Particularly, anti-androgenic activity can be evaluated as
CC indicative of therapeutic effects for prostate cancer, although any
CC compound which modifies the expression of a prostate-specific gene
CC may be considered a candidate compound.

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So Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 other;

Ouery Match

B83.5%; Score 42.6; DB 19; Length 12047;
Best Local Similarity 88.2%; Pred. No. 2.4e-06;
Matches 45; Conservative 1; Mismatches 5; Indels 0; Gaps

Oy 1 TCAAGACCAGCCAGACAACTGGAAGACCCGGTCTCTACAAAAAATACA 1935

Db 1985 TCAAGACCAGCCAACAAACCCCGTCTACAAAAAAAACA 1935
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Search completed: February 11, 2003, 02:04:45 Job time : 24.723 secs

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1 (bases 1 to 1669)
Raimundo,S. and Zanger,U.
Polymorphisms in the human cyp2d6 gene promoter region and their use in diagnostic and therapeutic applications
Patent: WO 0155432-A 1 02-AUG-2001;
                                                  AX207224 Sequence
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 from Patent WO0155432.
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                                OM nucleic - nucleic search, using sw model
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Kimura,S., Umeno,M., Skoda,R.C., Meyer,U.A. and Gonzalez,F.J.
The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Draft entry and computer-readable sequence for [Am. J. Hum. Genet. 45, 889-904 (1989)] kindly submitted by S.Kimura, 29-MAR-1990.
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Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
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           Length 9432;
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0218638-A 1 07-MAR-2002;
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tive 0; Mismatches 0;
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                                                                                                                                                                                Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Blocentre University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND 2 (Dassel to 13677)
Heim, M.H. and Meyer, U.A.
Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6 Genomics 14 (1), 49-58 (1992)
93052308
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 ( bases 1 to 13677)
Heim, M.H.
Direct Submission
                                           X58468.1 GI:30337
CYP2D7DB gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens.
Homo sapiens.
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Location/Qualifiers
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              // Commber:2
8675. .3224
// Capaca"CYP2D6"
// Inote="G00-132-127; does not fit consensus"
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JOURNAL
           AUTHORS
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Manna, Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burrows, J., Carter, M., Chacko, J., Chen, Z.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
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Forcum-Tansey, J., Frantz, P., Ganesh, R., Garcia, D. K., Gorrell, L.L., Guewara, M., Holloway, C., He, X., Hernandez, J.,
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Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O.,
Lozado, R.J., Lu, J., Lucier, R., Martin, R., Martinez, C., McLed, Mei, G., Moore, S., Moorish, T., Morgan, M., Naurine, S., Nash, S.,
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Nerestond, M., Weinstond, S.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 40; Conserv
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished, for Human and Mouse sequences.

Genes and Region of sequences similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons filanked by consensus splice sites that maintained sequence continuity across the splice Junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
Direct Vibraission
Submitted (27-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                        Submitted (28-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 27, 2000 His sequence version replaced gi:7331305.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
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ttttttgaga (t)ggagttttgc
tattctggtc(a)acatggtgaa
acatggtgaa(a)cctgtctct
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gcatgagaat(c)gcttgaacct
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Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus:
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                                                                                                                                                         4 (bases 1 to 170346)
Worley, K.C.
                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Features listing,
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gcttgaacct(g)ggaggcggaa

tcttgaaccn(n)ggaggcggaa

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PRI 09-JAN-2002
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Submitted (12-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172611)
Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, on oct 12, 2011 this sequence version replaced 91:15624993.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 1 MO 63108, USA
4 (bases 1 to 172611)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC019129 172611 bp DNA linear PRI 09-JA Homo sapiens BAC clone RP11-559M23 from 2, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
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Trani,L., Abbott,A. and Creason,K.
The sequence of Homo sapiens BAC clone RP11-559M23 (bmpublished (2001) 3 (bases 1 to 172611)
                                                                                                                                                                                                                                                                         Score 34.2; DB 9; Length 1
Pred. No. 0.033;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                 Db 75439 CCTGTCTCTACTAAAATACAAAAACCTAGGCGTGGTGGCA 75399
                                                                                                                                                                                                                                                                                                                                                 1 CCTATCTCTACTGAAAATAYAAAAGCTAGACGTGGTGGCA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: H_NH0559M23
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Waterston, R.
                                                                                                                                                                                                                                                                           ch • 83.4%;
1 Similarity 87.8%;
36; Conservative
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AC019129
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SOURCE
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                   ccagcctggg(t)gacagagcca
tatttattta(t)tttgagatga
                                                                                                                                                                                       gtatttttg(t)agaggcaggg
attttttgta(g)aggcagggtt
                                                                                                                                                                                                                                                           aaaacaaaaa(a)ctttagctaa
atgcttaata(a)gcttggagga
                                                                                                                                                                                                                                                                                                             gcatgatctc(g)gctcactgca
gagaaatgcc(a)tttaattttg
                                                                                                                                                                                                                                                                                                                                             aggtctttgg(t)gacttttgag
taggagaagc(a)tcaggaaatt
                                                                   ggatgttaag(t)aātgtāctga
ctaattcata(a)aatcattttt
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                                                                                                                     gccattcatt(c)aatctctacc
                                                                                                                                                       tgtatgagaa(c)caaagacaga
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                                                                                                                                                                                                                                                                                               ggcatgatct(c)ggctcactgc
                                                     gtattttttg(t)agagggtctt
                                                                                                                                       ccattcattc(a)atctctacct
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Phrap Value Range
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                                                   gtattttttg(n)agagggtctt
ggatgttaag(n)aatgtactga
ctaattcata(t)natcattttt
taattcata(n)atcattttt
                                                                                                                   gccattcatt(n)natctctacc
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Location/Qualifiers
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USA

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This sequence may not represent the entire insert of this
                            clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa.K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (Http://www.resgen.com) or pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacyac.med.buffalo.edu) SOURCE INFORMATION:

VECTOR: pBACC3...
NEIGHBORING SEQUENCE INFORMATION:
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC087053; the clone sequenced to the right is RP11-2415, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-559M23; actual end is at base position 17064 of RP11-2415.

Single plasmid coverage exists between bases 30202 to 30267 Location/Qualifiers

FEATURES

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148232
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159215
                                  TITLE
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       AUTHORS
                                                                                                                                       COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC079840 187486 bp DNA linear HTG 15-OCT-2001
Homo sapiens chromosome 3 clone RP11-316J16, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
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                                                                                                                                                                                                                                       Score 34.2; DB 9; Length 172611; Pred. No. 0.033;
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                                                                                                                                                                                                                                                                                          1; Mismatches
18006. .18289
/rpt_family-"Malk"
18361. .18553
/rpt_family-"L2"
18716. .18742
/rpt_family-" (TTTG)n"
19412. .19455
/rpt_family-" (TG)n"
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AC079840.8 GI:16117913
HTGS. HTGS_BHASE1; HTGS_DRAFT.
HOMO Saplens.
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87.8%;
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Best Local Similarity 87.8
Matches 36; Conservative
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AC079840
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KEYWORDS
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbark_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Direct Submission
Submitted (13-SEP-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11141921.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; L08821
Chemistry: Dye-terminator B1g Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 171757 bases at least Q40
Consensus quality: 171757 bases at least Q30
Consensus quality: 17812 bases at least Q30
Estimated insert size: 180914; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; sum-of-contigs cstimation
Quality coverage: 3.4x in Q20 bases; sum-of-contigs cstimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
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of 8625 bp in length
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(bases 1 to 187486)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  Gaps
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On Aug 13, 2002 this sequence version replaced gi:21747801.
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Center code Widesc

Web site:http://genome.wustl.edu/gsc/index.shtml

Contact: submissions@watson.wustl.edu

Contact: submissions@watson.wustl.edu
                                                                                                              bp in length
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                                                                                                                                                                                                                                                                                                               4; Indels
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Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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of 3084
                                                                                                                          gap of unknown contig of 2759
                             of 3916
              unknown
                                                                                                                                                                   1. .187486
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens clone
                                                                                                                                                                                                                            /clone="RP11-316J16"
39656 c 39493 g 5
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                          contig
gap of
contig
gap of
gap of
contig
contig
                                                                                                                                                       Location/Qualifiers
 contig
gap of
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                                                                                                                                                                                                                /chromosome="3
                                                                                                                                                                                                                                                                                   83.4%;
87.8%;
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Waterston, R.H.
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Waterston, R.H.
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Waterston, R.H.
                                         174792:
177876:
                                                                   177976:
180949:
                                                                                                                           184727:
187486:
                                                                                             181049:
                                                                                                               184627:
170676:
                          174692:
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Matches 36; Conserv
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174793
177877
177977
180950
181050
184628
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DEFINITION
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TITLE
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AUTHORS
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AC127379
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 170307)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Bortier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-APR-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS00002 170307 bp DNA linear PRI 26-APR-2
Human chromosome 14 DNA sequence BAC R-96617 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
AL049777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - Web : www.genoscope.cns.fr)
On May 15, 2000 this sequence version replaced gi:6468471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 207266,
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Consensus quality: 206829 bases at least Q40 Consensus quality: 207045 bases at least Q30 Consensus quality: 207263 bases at least Q20
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Pred. No. 0.032;
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/note="assembly_name:Contig8"
42249 c 42430 g 58438 t
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Contact: SeqRef@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-808E20"
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87.88;
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Matches 36; Conservative
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Direct Submission
Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 20, 2001 this sequence version replaced q1:14346133.
During sequence assembly date is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlapp as described above.
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Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALS91437 39528 bp DNA linear PRI 17-NOV-2003
Human DNA sequence from clone RP13-223M5 on chromosome X, complete
                                                                                                                                                                                                                                                                                   Submitted (31-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 31, 2002 this sequence version replaced 91:15022014. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NOTE: Shatter libraries failed to resolve repeat region 65151-65432. Unsure number of repeat copies 65151-65432. Forced join 65401."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39528)
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                                               1 (bases 1 to 210044) \, DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTE: Shatter libraries failed to resolve repeat region
65151-65432. Unsure number of repeat copies 65151-65432.
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/organism⊶"Homo sapiens"
/db_xref⊍"taxon:9606"
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/clone="CTD-2622113"
65151. .65432
/note="NOTE: Shatter
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                                                                                                                          2 (bases 1 to 210044)
DOE Joint Genome Institute.
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AL591437.6 GI:17017770
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Matches 35; Conservative
                                                                                  Direct Submission
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ORIGIN
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AL591437
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Identified using the e-PCR software (G. Schuler)"
94717. 95047
/note-"matching EMBL:X74142
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//note="matching EMBL:G32636
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Identified using the e-PCR software (G. Schuler)"
31571 c 31363 g 53061 t
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Identified using the e-PCR software (G. Schuler)*
95/67. 95916
//note="matching EMBL:D59942
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119069. .119269
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                                                                                                                                                                                                                                                                                     . 99 %.
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/note-"matching EMBL: H23232
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Organisme"Homo sapiens"

/db_xrefe"taxon:9606"

/chromosomee"14"

/clone="RF-96617"

/clone=11br="RPCI-11"

43803. .43927
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1. .170307
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Overall quality chart
Range : bases
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Direct Submission
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, database can be found at
                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RP13-223M5 is from the library RPCI-13.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone RP13-223M5 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP13-192B19 is at 37529 in this sequence. The true right end of clone RP1-314H24 is at 2000 in this
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3 (bases 1 to 103606)
Waterston, R.
Direct Submission
Submitted (14-JAN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 103606)
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103606)
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Homo sapiens PAC clone RP3-403E2 from 22, complete sequence.
AC005004
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/clone="RRP13-223M5"
/clone_lib="RRPC1-13.1"
a 7301 c 7036 g 12898 t
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Pred. No. 0.13;
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85.4%;
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outmitted (20-JAN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
(bases 1 to 103606)
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Dec 21, 1999 this sequence version replaced gi:6560935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  representation of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 22 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR22, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                     Washington
Missouri 63108, USA
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 103606)
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The clone may be obtained either from Genome Systems, Inc.
(http://www.genomesystems.com) or Research Genetics, Inc.
(http://www.resgen.com): or from Pieter de Jong.
VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RP3-403E2; actual start to fish of RP3-403E2.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                              Department of Genetics,
Park Avenue, St. Louis,
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Contact: sapiens@watson.wustl.edu
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/db_xref="taxon:9606"
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/clone_lib="RPCI-3"
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                                                                                                                                                                      Direct Submission
Submitted (11-DEC-1999)
                                                                                                                                                                                                                                                 University, 4444 Forest 6 (bases 1 to 103606)
Waterston, R.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (31-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2002 this sequence version replaced g1:9801261.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                          79.5%; Score 32.6; DB 9; Length 103606; illarity 85.4%; Pred. No. 0.13; Conservative 1; Mismatches 5; Indels 0;
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------ Project Information
Center project name: Y313F4
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18628. 18870
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Web site: http://www.sanger.ac.uk
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19703. 19943
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21844. .22137
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Matches 35; Conserve
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11765. .12066
                                                 903. 1198 / Trpt_fanlu" | 1381. 1689 / Trpt_famlly" | 1381. 1589 / Trpt_famlly" | 1384. 2139 / Trpt_famlu" | 1565. 2331
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2589. .12622
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[741. .11764
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3253. .13547
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3548. .13693
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                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be bepreserved.
                                                                                                                                                                                                                                Insert size: 366809; sum-of-contigs
Quality coverage: 6.13x in Q20 bases; sum-of-contigs
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Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ABI; 85% of reads Chemistry: Dye-primer-amersham; 10% of reads Chemistry: Dye-primer Big Dye; 3% of reads Consensus quality: 358581 bases at least Q40 Consensus quality: 362683 bases at least Q20 Consensus quality: 364911 bases at least Q20
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28048. 3298?
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/db_xref="taxon:9606"
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199658: contig of
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Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112088)
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2 (bases 1 to 112088)
Ricke, D.O.
Large Scale Sequence Analysis and Annotation with the Sequence
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Pred. No. 0.13;
1; Mismatches 5; Indels 0;
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179967. located
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//note-assembly_fragment:03581
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/rpt_family."L1" 3786538147 /rpt_family."Alu" complement(40345. /rpt_family."Alu"							/note="47167.	/rpt_family~"Alu" 4802548095	c	/rpt_family~"MIR" prim_transcript join(5220152421.5606356185)	/Scandard_danne="V1/3UV/ /note="84% identity mouse dbEST:AA498081" 5403 54735		/rpt_family-"Alu" /rpt_family-"Alu" reqion 5413354168		/rpt_unit=CT region complement(5519855325)	/rpt_family~"MIR" 5620356340	- 2	/note="99% identity dbEST:AA095819" 56941. :57036		/rpt_tamily~WHR" prim_transcript join(5862358971,5908959471)				/rpt_urype=randem /rpt_unit-AAAG		` ` `	•				/rpt_family="Alu" 6251462638	
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Comparison Analysis (SCAN) System Unpublished 3 (bases 1 to 112088) Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M.,	Rojeski, H., Subramanian, S. and Martin, C.H. Direct Submission Submitted (01-70L-1998) Human Genome Center, DOE Joint Genome	Lawrence Berkeley National Laboratory, MS /4-15/, .A 94720, U.S.A. Dmitted by:	Joint Genome Institute. Location/Qualifiers	1112088 /organism="Homo sapiens" /Ah vrefe"Havn.ofAff"	At Ct - Ct A C	/clore="BAC 282B7" /note="LBNL H192"	278400 /note="GRAIL 2 excellent exon, frame 1"	2655 family="Alu"	complement(60998811) /rpt_family="L1"	1078410913 Tytt family "MER45" 1057-7 .02.	o12013 e-"(ATGG)11" tVPG-tangem	/rpt_unit-ATGG complement(14548, .16322)	_family="L1" lement(1847218652)	_family="Alu" 8. 19074	/rpt_family="Alu" 1908919122	/note="(AC)17" /rpt_type=tandem	/rpt_dilteAc complement(1939), .19697)	_ramily="Alu" rement(50481, .20950)	/rpt_ramlly="L1" 2/2980. 2.3163 /cot 611		er (AC)24" jt	/ + pc_dnitc_nc complement(2468124880) /rof familyc=12480)	lement(238725503) familyc=MTD		4		/ift_dilt_1 Complement(1967329961) /rot family_ali,"	31039. 3131 7rot. family="Alu"	3248732904 /rpt familye"alu"	Complement(3)32833454) /rpt family="MRR"	635369 _family="L1"	3561735792
Comparison Ar JOURNAL Unpublished REFERENCE 3 (bases 1 a AUTHORS Kimmerly, W.,	TITLE Direct Submits JOURNAL SUBMITTEE (0)	INSTITUTE, LAWRENCE BE Berkeley, CA 94720, U.S COMMENT Sequence submitted by:	BOE S	source 1.						repeat_region 1078		/rpi				/no/	repeat_region comp	repeat_region comp	/rpl repeat_region 2296	repeat_region 2436	/rpt	repeat_region comp	repeat_region comp	repeat_region 2923	repeat_region 2969	/rpt	repeat_region comp	repeat_region 3103	repeat_region 3248	repeat_region comp	repeat_region 3527	repeat_region 3561

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/rpt_unit=T
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Search completed: February 11, 2003, 05:30:34 Job time: 277.088 secs

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 1 CCTATCTCTACTGAAAATAXAAAAGCTAGACGTGGTGGCG
 41

 Db
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 97244

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February 10, 2003, 21:06:50 ; Search time 141.088 Seconds (without alignments) 8457.264 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutcleostom1; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

ORGANISM

Risinger, C., Andersson, M.K., Lewander, T. and Ollasson, E. Detection of cyp2d6 polymorphisms Patent: WO 0218638-A 2 07-MAR-2002;

REFERENCE AUTHORS TITLE JOURNAL

ALG69860 Mouse DNA AC108967 Rattus no AC108162 Rattus no AL356794 Human DNA AC10241 Human Buscu AC012081 Homo sapi AC111097 Homo sapi PAT 18-MAY-2002 AX207224 Sequence AX34458 Sequence AX348144 Sequence AX348144 Sequence AX348144 Sequence AC111843 Rattus no AC111138 Mus muscu AC108309 Rattus no AC112075 Rattus no AC12070 Rattus no AC12090 Rattus no AC12090 Rattus no AC1089624 Rattus no AC1089624 Rattus no AC126935 Mus muscu AC126935 Mus muscu AC11089 Homo sapi AC117714 Mus muscu AC117089 Homo sapi AC117714 Mus muscu AC117089 Homo sapi AC117714 Mus muscu AC1089 Homo sapi AC117714 Mus muscu M33388 Human cytoc X58467 Human CYP2D X58468 Human CYP2D M33387 Human debri AL607074 Mouse DNA AC094607 Rattus no AL731665 Mus muscu Mus muscu Mus muscu AL844183 Mus muscu AL591146 Mus muscu AC115912 Mus muscu AX394457 Sequence M33189 Human debri AX394456 Sequence AL021878 Human DNA score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. linear DNA ALIGNMENTS Sequence 2 from Patent W00218638. AX394457 AX394457.1 GI:21065595 SUMMARIES HS257120
AX348344
AX362424
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AC1711138
AC172090
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AC138193 HUMCYP2D6 HSCYP2D7A HSCYP2D7B HUMCYP8P AX394457 HUMCYP2DG 62.9 136016 62.9 164176 62.9 164176 62.9 168738 62.9 204492 62.9 253913 62.4 41724 61.5 33918 61.5 33918 65.4 188353 64.4 194184 63.9 171777 17060 Length Query Match naman. RESULT 1
AX394457
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DEFINITION
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ORIGIN

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PAT 18-MAY-2002
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Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
M33388
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0218638-A 1 07-MAR-2002;
Gemini Genomics PLC (GB)
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/note="debrisoquine 4-hydroxylase intron H"
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3254. 3430
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Pred. No. 5.5e-06;
1; Mismatches 0;
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Pred. No. 5.3e-06;
1; Mismatches 0;
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Sequence 1 from Patent W00218638.
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/number=6
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Best Local Similarity 97.6%;
Matches 40; Conservative
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1537 c
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Matches 40; Conserv
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HUMCYP2D6
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KEYWORDS
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Draft entry and computer-readable sequence for [1] kindly submitted braft entry and computer-readable sequence for [1] kindly submitted by F.Gonzalez, 23 AMR-1990, for release after publication.

Author address: F.Gonzalez

National Cancer Institute
Bedg. 37 Rm. 38-24

National Institute of Health
Bethesda, Md 20892.

Location/Qualifiers

1. 5503

/organism="Homo sapiens"
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/note="debrisoquine 4-hydroxylase mRNA and introns"
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                                                                                                                                                                                                                                                                                                                                       HUMCYP2DG 5503 bp DNA linear PRI 27-APR-1993 Human debrisoquine 4-hydroxylase mutant allele (CYP2D6-MA1) gene, complete cds.
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PVPTTQTLGFGPRSQGKQRGYPGALMARVARAEALLKLHLAOLGPGGEVAGAVGRBR
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LARMELFLFTSLLQHFSFSVPTGQPRPSHHGVFAFLVTPSPYELCAVPR"
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Gonzalez, F.J.
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note="debrisoquine 4-hydroxylase intron
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                                                                                                                                                                                                                1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCTG 41
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                                                                                                                                           99.0%; Score 40.6; DB 6;
100.0%; Pred. No. 5.8e-06;
1ve 0; Mismatches 0;
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                                  1. .1680
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1 379 c 539 g 342
               Location/Qualifiers
                                                                                         539 g
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Human individual MAGA DNA.
Gemini Genomics PLC (GB)
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2572. .266
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HUMCYP2DG
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Submitted (25-Mar.1991) M.H. Heim, Dept of Pharmacology, Blocentre
University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND
2 (bases 1 to 13278)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13278)
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CXP2D7APp gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens
Homo sapiens
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Pred. No. 5.3e-06;
1; Mismatches 0; Indels
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Human CYP2D7AP pseudogene for cytochrome P450 2D6.
X58467
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Best Local Similarity 97.6%;
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                            1. .9432.
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1427. 4568,4776. 4963,5418. 5559,5658. 5909)
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PVPITQILGFGPRSQCYFLARYGPAWTEQRRFSVSTLRNLGLGKKSLEQWYTBEAACL
CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
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ABMEKAKGRPESSENDENLAIVVADLESAGWYTTSTTLAWGLLLMILHPDVQRRVQDE
IDDVIGQVRRPEMGDQAHMPYTTAVIHEVQRFGIVDLGVTHWTSRDIEVQGFRIPKG
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MELFLFFISLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 9432) (bases 1 to 9432) (bases 1 to 944.) Skoda, R.C., Meyer, U.A. and Gonzalez, F.J. The human debrisoquine 4 hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                                                                                 2574001
Draft entry and computer-readable sequence for [Am. J. Hum. Genet.
45, 889-904 (1989)] kindly submitted
by S.Kimura, 29-MAR-1990.
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M33388.1 GI:181303
cytochrome P450; cytochrome P450 IID6.
Human DNA, clone lambda2D-18/2.
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                                                           Homo sapiens
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jóin(1534. .1801,2504. .2675,3203. .3355,3444. .3605,
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Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND 2 (bases 1 to 13677)
Heim, M.H. and Mayer, U.A.
Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6
Genomics 14 (1), 49-58 (1992)
                                                                                                                                                                                                                                                                                                                      PRI 21-0CT-1992
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13677)
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CYP2D7BP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens.
Homo sapiens
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                                                                                                                                             Length 13278;
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Location/Qualifiers
1. 13677
1. 13677
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Human CYP2D7BP pseudogene for cytochrome P450 2D6.
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3651 - 3827,4020 - 4161,4356 - 4542,4998 - 5139,5238 - 5489)
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/gene="CYP2D7AP"
Heim,M.H. and Meyer,U.A.

Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6
Genomics 14 (1), 49-58 (1992)
93052308
                                                                                       See X58468, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
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/numberg
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3733, .13909,14102, .14243,14438, .14625,15080, .15221,
5320, .15496)
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Draft entry and computer-readable sequence for [1] kindly submitted by S.Kimura, 29-MAR-1990.

Location/Qualifiers
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Human DNA, clones lambda-2D-A and lambda-2D-B.
Human DNA, clones lambda-2D-A and lambda-2D-B.
Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 17060)
Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
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Am. J. Hum. Genet. 45 (6), 889-904 (1989)
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1031. .4207
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HUMCYP8P
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compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                         http://www.sanger.ac.uk/HGp/Chr22
RRP1-257120 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
This sequence is the entire insert of clone RPI-257120 The true
right end of clone RPI-18601 is at 20171 in this sequence.
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//note="match: GSS: Em:AQ124532"
//note="match: GSS: Em:AQ124532"
//note="match: GSS: Em:AQ124532"
//note="Limb repeat: matches 1. .1057 of consensus"
//note="Limb repeat: matches 1552. .1964 of consensus"
//note="Limb repeat: matches 1482. .1552 of consensus"
//note="Limb repeat: matches 122. .1482 of consensus"
//note="Limb repeat: matches 1222. .1482 of consensus"
//note="Consensus"
//note="Consensus"
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19896. .19939
20.246. .20284
/note="Lip repeat: matches 2416.
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/note="LIP repeat: matches 2311.
20965. .20982
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21270. .22130
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/clone_lib="RPCI-1"
1093. .1682
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/note="match: STS: Em:HS324WC5"
7972. .9283
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/note="match: GSS: Em:AQ563517"
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/note="match: GSS: Em:AQ684484"
7162. .7366
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7357, 7396
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/db_xref="RZPD:RPCIP704120257"
/db_xref="taxon:9606"
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/note="match: STS: Em:G07321"
25597. .26083
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9981. .10378
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/note="CpG island"
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Cambridgeshirs, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 25, 2001 this sequence version replaced gi:3204432.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
rogether with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORNMPEP; Information
on the WORNMEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was finished as follows unless otherwise noted: all regions were
either double-stranded or sequenced with an alternate chemistry or
attempt was made to resolve all sequencing problems, such as
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human DNA sequence from clone RP1-257120 on chromosome
22q13.1-13.2, complete sequence.
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                                                                 /pseudo
13147. .13307
/gene="CYP2D7"
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/gene="CYP2D7"
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/gene="CYP2D7"
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/gene="CYP2D7"
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ALO21878.2 GI:17065905
12906. .13058
/gene="CYP2D7"
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/gene="CYP2D7'
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/gene="CYP2D7"
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Matches 40; Conservative
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37324. .37437
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="HERVI repeat: matches 1561. .2163 of consensus" 31873. .33456
/note="HERVI repeat: matches 9. .1561 of consensus" 33464. .33959
/note="LTR10B repeat: matches 1. .510 of consensus" 33960. .34110
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37163. .37323
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//4417...54450
//4417...54450
//note-will copies 2 mer ca 100% conserved"
54578...15083
//note-will repeat: matches 30...587 of consensus"
//note-will repeat: matches 30...587 of consensus"
//note-will repeat: matches 30...587 of consensus"
//note-will repeat.
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44916. 45564
//note-"LTR12 repeat: matches 5. .671 of consensus
48350. .99467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /notes "57 copies 2 mer ga 79% conserved" complement(join(42379, 42591,42916, 43112)) /notes "match: STS: Em:G2750%" complement(join(42491, 42603,42916, 42945)) /notes "match: STS: Em:G43129" 43992 , 44915
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// Anotes match: GSS: Em: AQ035975"  
// Anotes match: GSS: Em: AQ035975"  
// Anotes match: G5929. .66550)  
// Anotes match: STS: Em: G27630"  
// Anotes match: STS: Em: G27630"  
// Anotes match: GSS: Em: AQ017313"  
// Anotes match: GSS: Em: AQ084812"  
// Anotes match: GSS: Em: AD084812"  
// Anotes match: GSS: Em: AD084812"
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30843. .30912
/notem"HERVI repeat: matches 2098. .2
30902. .30971
/notem"HERVI repeat: matcher
                                                      complement(26269. 26446)
/note="match: GSS: Em:AF046780"
26890. 26995
/note="match: GSS: Em:AZ083430"
27147. 28076
/note="HERVI repeat: matches 4455...
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30961. 31556
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/note="match: GSS: Em:AQ389013"
complement(78421. .78533)
/note="match: GSS: Em:AQ042556"
complement(78451. .78977)
/note="match: GSS: Em:AQ533248"
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Em: B13982"
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artificial sequences.

I (bases I to 1669)
Raimundo,S. and Langer,U.
Polymorphisms in the human cyp2d6 gene promoter region and their use in diagnostic and therapeutic applications
Petent: WO 0155432-A I 02-AUG-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="artificial sequence"
a 376 c 534 g 338 t
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Sequence 529 from Patent WO0200928.
AX345458
AX345458.1 GI:18493344
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Matches 40; Conservative
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Matches 39; Conserv
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Worley, K.C.
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TITLE
JOURNAL
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AC097793.4 GI:21723633
HTG; HTGG.21723633
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                       Journey, Jou
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo saplens)"
1 92 c 1514 g 3019 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                         Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 529 03-JAN-2002; Epigenomics AG (DE)
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Pred. No. 0.028;
1; Mismatches 5; Indels 0
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AX348344
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Location/Qualifiers
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85.0%;
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                             artificial sequences.
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Best Local Similarity
Matches 34; Conserv
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BRONK J., Bowde, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
BROWG, C., Bowde, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Charton, T., Carter, M. Hartherions Branchist, E., Bridgeld, C.,
Chen, G., Chen, S., Chen, Z., Chordhy, T., Christopoulavazi,
Chen, G., Chen, S., Chen, Z., Coyle, M.D. Datherine, S.P. David, R.,
Davila, M.L., Dauly, Y., Din, H.,
Davila, M.L., Dauly, Y., Din, H.,
Davila, M.L., Dauly, D., Elagon, D., Elagon, M., Datherine, S.P. David, R.,
Garrell, M. Gody, Carter, M., Danger, C., Elbaj, C., Esotto, M.,
Garrell, T., Ferraguto, D., Elagon, N., Edayari, C., Esotto, M., Chill, R.,
Harris, C., Harris, R., Harry, M., Bord, N., Din, H., H.,
Harris, C., Harris, R., Harry, M., Brown, M., Dillowa, M., Mollowa, M
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arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H.,

Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Martinez, E.,

Maheshwari, M., Mapua, P., Martin, R., Machindale, A., Martinez, E.,

Miner, G., Miner, Z., Mitchell, T., Monabbat, K., Moryan, M.,

Miner, G., Miner, Z., Mitchell, T., Monabbat, R., Moyen, N.,

Noven, N., Novedo, P., Pater, P., Paten, P., Er, Oulles, M., Ren, Y.,

Raves, M., Notedo, R., Pace, A., Patton, B., Peery, J., Perez, L.,

Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stson, I.,

Scherer, S., Scott, G., Shen, H., Shooshtari, N., Thomas, S.,

Usmanl, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Thongs, V.,

Walliams, G., Williamson, A., Waleczyk, R., Wooden, S., Worley, K.,

Williams, G., Williamson, A., Wileczyk, R., Wooden, S., Worley, K.,

Nirek, Suhmission
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 109 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-UL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2002 this sequence version replaced gi:18701687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 87903 bases at least Q40
Consensus quality: 95337 bases at least Q20
Consensus quality: 101488 bases at least Q20
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1121: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
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Center project name: GOIS
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Worley, K.C.
Direct Submission
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Direct Submission
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COMMENT

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Biren, 320 Charles Street, Cambridge, MA U2141, USA

Staten, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Bairen, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Burkhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chung, J.,

Chazaro, B., Cookel, Y., Colangelo, M., Collins, S., Collymorc, A.,

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Oliver, J., Peterson, K., Phunkhang, P., Pierro, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Riley, R., Schupback, R.,

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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Direct Submission, E., Zimmer, A. and Sody, M.,

Direct Submission, E., Zimmer, A. and Sody, M.,

Direct Submission, E., Zimmer, A. and Sody, M.,

Direct Submission, E., Zimmer, A. and Sody, M.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Steuman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Myman, D., Ye, W.J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 15, 2002 this sequence version replaced 91:18699883.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                  Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Rescurch
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This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 194000; agarose-fp
Insert size: 192484; sum-of-contigs
Quality Coverage: 6.6 in Q20 bases; agarosc-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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1 4349; contig of 4349 bp in length
4450 4449; gap of 6438; contig of 1989 bp in length
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Mus musculus clone RP23-364J12, WORKING DRAFT SEQUENCE, 18 ordered
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Gord, S., Gord, E., M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Langazares, R., Lamazares, R.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 194184)
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Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Marquis, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Naylor, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
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Pred. No. 2.2;
1; Mismatches 8; Indels 0;
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gap of unknown length
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-364J12
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                      contig of 1051 b
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Best Local Similarity 77.5%;
Matches 31; Conservative
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67006 67105: gap of 67100 bp 67106 114741: contig of 47636 bp in length 114742 137081: contig of 6720240 bp in length 137082 137181: gap of 100 bp 137182 181365: contig of 44184 bp in length 181366 181465: gap of 100 bp 100 bp 181366 194184: contig of 12719 bp in length.
                                                                                                                                                                                                                                                                                                                                                  63: gap of 100 bp 67005: contig of 11042 bp in length
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100 bp
of 2348 bp in length
                             100 bp
of 3855 bp in length
                                                              12842 12941: gap of 100 bp
12942 15693: contig of 2752 bp in length
                                                                                          15694 15793: gap of 100 bp 15794 18535: contig of 2742 bp in length
                                                                                                                         18536 18635: gap of 100 bp
18636 21710: contig of 3075 bp in length
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AC073151 171777 bp DNA linear HTG 15-MAY-2002 Mus musculus clone RP23-234E13 strain C57BL6/J, WORKING DRAFT SEQUENCE, 32 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 17177)

Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Ioshikhes I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUN-2000) Department of Molecular Genetics, Albert bistein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA On Aug 9, 2001 this sequence version replaced gi:15027676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 17177)
Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R.,
Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A.,
Gordon, M., Goltz, J.S. and Kucherlapati, R.
Direct Submission
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Mus musculus.
Mus musculus
                                                             clone_end:T7
                                                                                                                                                             64.48;
78.98;
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Best Local Similarity 78.99
Matches 30; Conservative
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JOURNAL
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AUTHORS
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gap of unknown length
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                                                               unknown length
of 8146 bp in length
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ö Gaps 63.9%; Score 26.2; DB 2; Length 171777; 75.6%; Pred. No. 3.9; Live 1; Mismatches 9; Indels 0; 658 others Db 138859 CTTTGTGTGTGTATTCGTGCATGTGTGTGCGTGTGCCTG 138899 1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41 /notee"assembly_name:Contig67"
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AX394456 Sequence M33388 Human cytoc X58468 Human CYP2D AL021878 Human DNA

AX207224 Sequence AX394457 Sequence

Description

SUMMARIES

Human cytoc Human CYP2D

Mus muscu Mus muscu Homo sapi Sequence

Sequence

AX078286 S AX156560 S AL136564 B AK056443 B

Homo sapi Homo sapi Homo sapi Homo sapi

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synthetic construct.
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[ (bases 1 to 1669)
Raimundo,S. and Zanger,U.
Rolymorphisms in the human cyp2d6 gene promoter region and their use in diagnostic and therapeutic applications
patent: WO 0155432-A 102-ANG-2001;
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AC124466
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AC069565
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Compugen Ltd.
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          GenCore version
Copyright (c) 1993 - 2003
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41
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Maximum Match 100%
Listing first 45 summaries
                                                           nucleic search, using sw model
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PAT 30-AUG-2001

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ALIGNMENTS

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join[1620. .1799,2503. .2674,3225. .3377,3466. .3626,
4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5836)
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CAAFANHSGRPFRDNGLLDKAVSNVIASLTGGRRFEYDDPRFLRLLDLAGEGLKEESG
                                                                                                                                                                                                                                                                                                                                                                      Eukarrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (base) 1 to 9432)
Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Draft entry and computer-readable sequence for [Am. J. Hum. Genet. 45, 889-904 (1989)] kindly submitted by S.Kimura, 29-MAR-1990.
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Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
M33388
            Score 40.6; DB 6; Length 9432;
Pred. No. 0.00076;
1; Mismatches 0; Indels 0
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Am. J. Hum. Genet. 45 (6), 889-904 (1989)
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cytochrome P450; cytochrome P450 IID6.
Human DNA, clone lambda2D-18/2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0218638-A 2 07-MAR-2002;
Genini Genomics PLC (GB)
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Patent: WO 0218638-A 1 07-MAR-2002;
Gemini Genomics PLC (GB)
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1. .9432
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SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutcleostom1;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutcleostom1;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutcleostom1;

Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Solved: Cassos 1 to 13677)

Eulem, M. H.

Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND

Evolution of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND

Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6

Genomics 14 (1), 49-58 (1992)

Ellistry Commission Com
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X58468.1 GI:30337
CYP2D7BP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 See X58467, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
1. .13677
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Human CYP2D7BP pseudogene for cytochrome P450 2D6.
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3356. .3443
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Pred. No. 0.00076;
1; Mismatches 0; Indels 0
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Best Local Similarity 97.6%;
Matches 40; Conservative
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HSCYP2D7B
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    RPI-257120 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pCYPAC2 This sequence is the entire insert of clone RPI-257120 The true right end of clone RPI-18601 is at 20171 in this sequence.
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/note="MER11C repeat: matches 1. .1057 of consensus"
16086. 16507
/note="Libor repeat: matches 1552. .1964 of consensus"
17055. .17127
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20246. .20284
/note="Lip repeat: matches 2378. .2416 of consensus"
20594. .20660
20594. .z0660
20965. .20982
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7162 .7356
/note="match: STS: Em:HS324WC5"
7357 .7396
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/note="match: GSS: Em:AQ563517"
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/note="match: GSS: Em:AQ124532"
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26890. .26995
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25597, 26083
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25611, 25853
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9981. .10378
                                                                                                                                           Location/Qualifiers
1. .114846
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/note="CpG island"
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Libert Submiston

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 25, 2001 this sequence version replaced gi:3204432.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information

thtp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was finished as follows unless otherwise noted: all regions were

covered by high quality data (i.e., phred quality >= 30); an

attempt was made to resolve all sequencing problems, such as

plasmid subclone or more than one M13 subclone; and the assembly

was confirmed by restriction digest. This sequence was generated

from part of bacterial clone contigs of human chromosome 22,

constructed by the Sanger Centre Chromosome 22 Mapping Group.

Further information can be found at

http://www.sanger.ac.uk/HGP/Ch122
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 114846)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%; Score 40.6; DB 9; 97.6%; Pred. No. 0.00071;
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/note="ACCCTTCCCC"
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5519. .5616
/gene="CYP2D7BP"
                                              /number=6
4735. .4922
/gene="CYP2D7BP"
1541. .4734
/gene="CYP2D7BP"
                                                                                                                                           4923. .5376
/gene="CYP2D7BP"
                                                                                                                                                                                                               5377. .5518
/gene="CYP2D7BP"
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/gene="CYP2D7BP"
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Matches 40; Conservative
                                                                                                                       'number=7
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Direct Submission
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ORIGIN

COMMENT

SOURCE

Gaps

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AC102388 163856 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP24-298F19, WORKING DRAFT SEQUENCE, 19
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boquslavkiy,L., Bukhgalter,B.,
Camarta,J., Chang,J., Characro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Dlaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
/note~"MER21B repeat: matches 686. .794 of consensus" 83910. .84357
/note«"MER21B repeat: matches 76. .540 of consensus" 85375. .85430
                                                                                                                                                                                                                                                                                                               Length 114846;
                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                    /note="11 copies 2 mer ac 100% conserved" 9274. 99444
/note="Other. Weak data"
104028. 104091
/note="32 copies 2 mer aa 67% conserved"
/note="az copies 2 mer aa 67% conserved"
/note="amatch: GSS: Em:AQ572846"
                                                                                                                                                                                                                                                                                                           Score 34.2; DB 9; Length 1
Pred. No. 0.069;
1; Mismatches 4; Indels
                                                                              conserved"
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                         1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                            /note:"28 copies 2 mer aa 76%
                                                                                              complement(90629, .90900)
/note="match: GSS: Em:B13983"
96343, .96364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-298F19 Unpublished
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Best Local Similarity 87.8%;
Matches 36; Conservative
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AC102388
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                                                                                                                                                                                                                                                                                                                                                                 note"Harleguin repeat: matches 912. .1086 of consensus"
37324. .37437
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/note="Link5A repeat: matches 5857. .6292 of consensus"
83609. .83702
/note="MER218 repeat: matches 703. .787 of consensus"
83697. .83797
                                                                                                                                                                                                        /note="HERUT" repeat: matches 9. .1561 of consensus" 33464. .33959
/note="LIRROND repeat: matches 1. .510 of consensus" 33960. .34110
/note="LIPBa repeat: matches 1226. .1378 of consensus" 34415. .35367
/note="LIPBa repeat: matches -656. .1226 of consensus" 37163. .37323
                                                                                              matches 2098. .2163 of consensus"
                                                      .4455 of consensus"
                                                                                                                                                          HERVI repeat: matches 1561. .2163 of consensus' .33456
              IRRVI repeat: matches 4455. .5408 of consensus<sup>1</sup>
30853
                                                                                                                                      consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note-"MER77 repeat: matches 30. .587 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .671 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .93 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                     /note="57 copies 2 mer ga 79% conserved"
complement(join(42379, 42591,42916, 43112))
/note="match: STS: Em:G27508"
complement(join(42491, 42603,42916, 42945))
/note="match: STS: Em:G43129"
                                                                                                                                    .2163 of
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65330. .66802
/noter"match: GSS: Em:AQ617313"
66577. .66930
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complement(69196. .69374)
/notes="match: GSS: Em:B14383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'noten"23 copies 2 mer tt 82% conserved"
                                                  /note="HERVI repeat: matches 2098.
30843, .30912
                                                                                                                                    matches 2098.
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/note."CpG island"
/evidence.not_experimental 54417. .54450
/note."17 copies 2 mer ca 100% con 54578. .55083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ181535"
complement(7878; ..78531)
/note="match: GSS: Em:AQ389013"
complement(78421. ..78533)
/note="match: GSS: Em:AQ042556"
complement(78451. ..78977)
/note="match: GSS: Em:AQ042548"
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/notee"pTR5 repeat: matches 40.
44916. .45564
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66603
/notee "match: GSS: Em:AQ044403"
66974. 67017
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35916. .65961
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/note="match: GSS: Em:AQ618257"
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/note⊷"match: STS: Em:G27630"
66514. .66549
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                                                                                                                                  /note="HERVI repeat:
30961. .31556
                                                                                          note-"HERVI repeat:
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/note-"CpG island"
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                                                                                                                                                              /note="HERVI
31873. 33456
                                                                                                                              'note="HERVI
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COMMENT

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HTG 18-JUL-2002
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                                                                                     10158 101457: contig of 26100 bp in length 101458 101457: contig of 26100 bp in length 101458 101557: gap of 100 bp 101558 126284 126284 126384 1255823: contig of 29440 bp in length 126384 1255823: contig of 29440 bp in length 100 bp
35805 35904: gap of 100 bp
35905 43468: contig of 7564 bp in length
43469 43568: gap of 100 bp
43569 75257: contig of 31689 bp in length
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                                                                                                                                                                                                                                 4 155923: gap of 100 bp 4 163856: contig of 7933 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-24 Male Mouse BAC"
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6552. .8978
/note="assembly_fragment"
9079. .11520
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41088 a 39986 c 39793 g 41185 t
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Pred. No. 34;
0; Mismatches
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13882. 16379
/note="assembly_fragment"
16480. 19552
/note="assembly_fragment"
19653. 24331
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/note="assembly_fragment"
29812. .35804
/note="assembly_fragment"
35905. .43468
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
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155924. .163856
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/note="assembly_fragment"
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note="assembly_fragment"
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43569. .75257
                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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Best Local Similarity 79.5%;
Matches 31; Conservative
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155924 16385
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AC127560
LOCUS
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  Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLaan, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mapu, C., Morran, C.H., O'Connor, T., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Vesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061474.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 118672
Center clone name: 298 F_19
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157585 bases at least Q40
Consensus quality: 167585 bases at least Q40
Consensus quality: 160552 bases at least Q30
Consensus quality: 161468 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 162056; sum-of-contigs
Quality coverage: 6.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contect: sequence_submissions@genome.wi.mit.edu
------- Project Information
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13781: contig of 2161 bp in length
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29711: contig of 5280 bp in length
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35804: contig of 5993 bp in length
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16379:
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24332
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JOURNAL
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Gaps

Gaps

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PRI 22-AUG-2001

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/producte"Unknown (protein for IMAGE:4153436)"
/protein_ide"AAH12882.1"
/db_xxefe"(01:15277574"
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DCQLLPEHRWITGGLIRVGAFCATPPNARGGRVKAAAAVFEDCPGWAARKAKRTPASR
PSARRTPIKGRQCGADKVGKEKGRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 19 Row: p Column: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (20-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCW-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garci
A.M., Holloway, M., Telford, B. Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Brain, anaplastic oligodendroglioma with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Day: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                             Length 232603;
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Homo sapiens, clone IMAGE:4153436, mRNA, partial cds.
BC012882
                                                                                                                                                                         533 others
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8
                                                                                                                                                                                                                                               Score 24.8; DB 2;
Pred. No. 94;
                    feature 97435. 169505.
/note-"assembly_name:Contigl4"
169606. 232395
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232496. 232863
/note-"assembly_name:Contigf5"
67248 a 46673 c 47059 g 71090 t
                                                                                                                                                                                                                                                                                                                                               4 AAGCAGTGGAGGAGGACRACCCTCAGGCAGCCGGGAG 41
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/clone_lib~"NCI_CGAP_Brn67"
/lab_host~"DH108"
                                                                                                                                                                                                                                                                                               1; Mismatches
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/clonee"IMAGE:4153436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                               60.5%;
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Strausberg, R.
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Matches 29; Conservative
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                                                                           misc_feature
                              misc_feature
                                                                                                                         misc_feature
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McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (17-UUL-2002) Genome Sequencing Center, 4444 Forest Park
J (bases 1 to 232603)
McPherson, J.D. and Waterston, R.H.
McPherson, J.D. and Waterston, R.H.
Submission
Submitted (18-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, W0 63108, USA
On Jul 18, 2002 this sequence version replaced gi:21886990.
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 232603)
MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
Mus musculus chromosome UNK clone RP24-267118, WORKING DRAFT SEQUENCE, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                    AC127560.2 GI:21903649
HTG; HTGS_PHASE1; HTGS_FULLTOP
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/note:"assembly_name:Contigll"
12499. .51823
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51924. .97334
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20-MAR-2002

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QGNLLKVIPAAAFQGVPHLTHLDLRHCEVELVAEGAFRGLGRLLLLNLASNHLRELPO
BALDGLGSLRRLELEGNALEELRPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVR
WLRLSNNALSVLAPEALAGLPALRRLSLHHNELDALECPVLSQARGLARLELGHNPL.
YGGEBGALALPGLRELLLDGGALQALGPRAFAHCPRLHTLDLRGNQLDTLPPLQGFQG
LRRLRLQGIRGGAARRGPTRVAGAARACHCRRVPGFRLRCEALDALRPWDLRCPGD
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VPRGFPSDTQLLDLRNHHFPSVPRAAFPGLGHLVSLHLQHCGIAELEAGALAGIGRLI
                                                                                                                                                            YLYLSDNQLAGISAAALAGVPRLGYLYLERNRFLQVPGAALRALPSLFSLHLQDNAVD
RLAPGDLGRTRALRWYYLSGNRITEVSLGALGPARELEKLHLDRNQLREVPTGALEGL
PALLELQLSGNPLRALRNGAROPVGRSEJGHLFUNSSGLEGOTFGRFSGLGPGLGSLHL
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GQRVKAAAAVFEDCPGWAARKAKRTPASRPSARRTPIKGRQCGADKVGKEKGCL"

9 22 c 876 g 431 t 4 others
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Martinsried GERNANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@kf2-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKF2P761141) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3071)
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/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DB108; sites Not1 + Sal1"
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1. .3071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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Pred. No. 2.7e+02;
1; Mismatches 10;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DKFZp761I141"
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1 Similarity 73.2%;
30; Conservative
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1 (bass 1 to 2553)
Hillman,J.L., Lal,P., Tang,Y.T., Yue,H., Au-Young,J., Bandman,O., Azimzai,Y., Yang,J., Lu,D.A., Baughn,M.R., Patterson,C. and Shah,P. Cell cycle and proliferation proteins
Patent: WO 0107471-A 90 01-FEB-2001;
Incyte Genomics, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 22-JUN-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2636)
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/note="Incyte ID No: 1868749CB1"
709 c 722 g 547 t
                                                                  Score 24.6; DB 9;
Pred. No. 3.7e+02;
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Matches 30; Conservative
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PRI 18-JAN-2002

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TGQLADGTPTGQDALVIGEDWGKELKHISYKAARVSCFKHVPLYDQWEDVMCKHKVPV

LNIBDAVLPSRYYWIASYIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPTGWCA IN

SALLVPPRTTHAKFTDWGCYLMKLVGSRTLPVDFHIKMYESMKYPFROGMRLEVVDK

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QFGKKKRKIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEHLLDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mekprsidetpssepmededoddetkggydsfrsynssygses
SSYLEESSEAENEDREAGELPTSPLHLLSPGTPRSLDGSGSEPAVCEMCGIVGTREAF
FSKTKRFCSVSCSRSYSSNSKKASILARLQGKPPTKKAKVLHKAAWSAKIGAFLHSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-JAN-2001) Wismar J., Johannes Gutenberg Universitaet, Institut fuer Genetik, Becherweg 32, 55099 Mainz, GERMANY Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              HSA305226 3194 bp mRNA linear PRI 18-JAN-200
Homo sapiens mRNA for H-1(3)mbt-like protein, alternative variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ305226.1 GI:13940238 alternative splicing; H-1(3)mbt-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular characterization of h-l(3)mbt-like: a new member of the
                                                      Length 3188;
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                                                                                                                                                                                          1988 AGAAGCCCTGCTGGAGGACGACCCTCAGGGTGCCAGGAAG 2028
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/protein_id="CAC37794.1"
/db_xref="GI:13940239"
                                                                                                                                                               1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCGGGAG 41
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                                                      Score 24.6; DB 9;
Pred. No. 2.6e+02;
1; Mismatches 10;
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Pred. No. 2.6e+02;
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/note="alternative variant a"
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FEBS Lett. 507 (1), 119-121 (2001)
21538645
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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40. .2157
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73.2%;
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                                              LNSDAVLPSRYWINSYLOTARY STRUCKS GENDAGIBEWCKLICTOWN TO SKILVPERTHAKFYDWKGYLLKYGERLDAGIBEWCKLICTOWN TO SKILVPERTHAKFYDWKGYLMKRLVGSRTLPVDFHTKMESMKYPROGMRLEVUN SQVSRTRAVDTVIGGERLLYZDGOSDDDFWCHMWSPLIHPVGWSRNGHGIKMSE RRSDAMHPFRRITCODAVPYLFKYRKANYTEGGWFEEGMKLEAIDPLULGKICVATV CKVLLDGYLMICVDGOPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTF NWBNYLEKTKSKAAPSRLFNMCPRHOFKYGKKLAYOKKLLAYDLMEPRLICYATVKRVYHKLL SIHFDGWDSEYDQWDCESPDIYPVGWCELTGYQLOPPVAAGVGSRGPKRL"

3052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3188 bp mRNA linear PRI 01-AUG-2002 no saptens cDNA FLJ31881 fis, clone NT2RP7002829, weakly similar Scm-related gene containing four mbt domains.
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FSKTKRFCSVSCSRSYSSNSKKASILARLQGKPPTKKAKVLHKAAWSAKICAFLHSQG
TGQLADGTPTGQDALVLGFDWGKFLKDHSYKAAPVSCFKHVPLYDQWEDVMKGMKVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamanoto, J., Isono, Y., Kawai Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Wagatsuma, M., Murakawa, Y., Kanehori, K., Yakahashita, H., Kanda, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Magai, R. and Isogai, T., Sugano, S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/cell_type="teratocarcinoma"
/clom_lib="NT2RP7"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 5-weeks retinoic acid (RA) induction."
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Oligo capping; fis (full insert sequence).
Homo sapions teratocarcinoma cell_line:NT2 cDNA to mRNA, clone_lib:NT2RP7 clone:NT2RP7002829.
                                                                                                                                                                                                                                                                                                                                                                    Score 24.6; DB 9; Length 3071;
Pred. No. 2.7e+02;
1; Mismatches 10; Indels 0
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2 (bases I to 3188)
1 (sogal, T., Otsuki, T. and Sugiyama, T. Direct Submission
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/db_xrefe"taxon:9606"
/clonee"NT2RP7002829"
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882 c 858 g
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Best Local Similarity 73.2%;
Matches 30; Conservative
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                                       Homo sapiens, hypothetical protein DKFZp7611141, clone MGC:2476 BC017191
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrone-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho.S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plates 4 Row: b Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13899349. Location/Qualifiers
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SYLEESSEAENEDREAGELPTSPLHLLSPGTPRSLDGSGSEPAVCEMCGIVGTREAF
SYLEESSEAENEDREAGELPTSPLHLLSPGTPRSLDGSGSEPAVCEMCGIVGTREAF
SYRTKRECSVSCSRSYSSNSKRASILARLOGKPBTKKANVLHKAAMSKITGAFLASOG
TGQLADGTPTGQDALVLGFDWGKFLKDHSYAAAPVSCFKHVPLYDWGDWDWWGWKVEV
INSDAVLPSRVYWIASVIQTAGYRVLLKYEGFENDASHBFWCNLGTVDVHPTGWCALN
SQVSRTRWAVVDTVIGGRLRLLYEGDSDDDFWCHWMSPLIHEVGWSRYSFGGRIKMSE
RRSDMAHHPTFRKITVDAVVYLGSRLRVYPEGGWFEGGMELEADDLNLGNICVATV
CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPRKGYEAQFF
WRNYLERFKKSRAAPSRLFNMCPHGFRYGNASHAIFPATFCQKNDIELTPPRKGYEAQFF
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OFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVA
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3222)
                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg,R.

Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Saglensburg, Maryland;
Web site:
Whitp://www.nisc.nih.gov/
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/protein_id="AAH17191.1"
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/Ob_xref="LocusID:83746"
/Ob_xref="taxon:9606"
/clone="MGC:2476 IMAGE:3138444"
/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIHAGC_21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 2.6e+02;
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                                  60.0%;
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Compugen Ltd.
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Copyright (c) 1993 - 2003
                                                                          US-09-942-310-2_COPY_860_900
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Maximum Match 100%
Listing first 45 summaries
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AX394456 Sequence
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X58467 Human CYP2D
X3451878 Human DNA
AX345458 Sequence
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synthetic construct
artificial sequences.
1 (bases 1 to 1669)
Raimundo, S. and Zanger, U.
Polymorphisms in the human cyp2d6 gene promoter region and their use in diagnostic and therapeutic applications
Patent: WO 0155432-A 1 02-AUG-2001;
                                     Description
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SUMMARIES
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AX207224 AX207224.1 GI:15394976
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689. .702
726. .5103
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LARMELFLFTSLLQHFSFSVPTGQPRPSHGVFAFLVTPSSPYELCAVPR"
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/note="debrisoquine 4-hydroxylase intron
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/note="debrisoquine 4-hydroxylase"
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/db_xref="GI:181306"
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1 (bases I to 5503)
Gonzalez, F.J.
Unpublished (1990)
Draft entry and computer-readable sequence for [1] kindly submitted by F. Gonzalez, 23-MaR-1990, for release after publication.

National Cancer Institute
Bidg. 37 Rm. 3E-24
National Institute of Health
Bethesda, Md 20892.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Risinger, C., Andersson, M.K., Lewander, T. and Oliasson, E. Detection of cyp2d6 polymorphisms
Patent: WO 0218638-A 2 07-MAR-2002;
Gemini Genomics PLC (GB)
Location/Qualifiers
                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                 Length 1669;
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                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                    860 GTGTGAGAGAATGTGTGCYCTAAGTGTGTGAGTCT 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                               ch 99.0%; Score 40.6; DB 6; 1 Similarity 100.0%; Pred. No. 5.9e-06; 41; Conservative 0; Mismatches 0;
                                  1. .1bb9
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/note="artificial sequence"
a 376 c 534 g 338 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%; Score 40.6; DB 6; ilarity 100.0%; Pred. No. 5.9e-06; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
379 c 539 q 34:
                                                                                                                                                                                                                                                                                                                             Sequence 2 from Patent W00218638.
AX394457
Biotechnologie AG (DE)
               Location/Qualifiers
1. .1669
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Human individual MAGA DNA.
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Best Local Similarity
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HUMCYP2DG
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AX394457
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SOURCE
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/dr_xrefe
/dr_xrefe"GI:181304
/dr_xrefe

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/geneლ"CYP2D6"
/notem=600-132-127; does not fit consensus"
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/gene="CYP2D6"
/note="GO0-132-127"
/number=3
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/note="G00-132-127"
/number=5
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/note="G00-132-127"
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/note="G00-132-127"
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/note="G00-132-127"
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/note="G00-132-127"
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4427. 4568
/gene="CYP2D6"
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/gene="CYP2D6"
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5658. .5909
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4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5836)
/gene="CYP2D6"
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Eukaryota...
Bukaryota...
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hobses I to 9432)

Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.

The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable sequence for [Am. J. Hum. Genet. 45, 889-904 (1989)] kindly submitted by S.Kimura, 29-MAR.1990.

Location/Qualifiers
                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/map-"22q13.1"
join(1532. 1799,2503. .2674,3225. .3377,3466. .3626,
4000. .42654427. .4568,4776. .4963,5418. .5559,5658.
/gene="CYP2D6"
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/gene="CYP2D6"
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                                                                                                                                                                                                                                                                           Risinger, C., Andersson, M.K., Lewander, T. and Oliasson, E. Detection of cyp2d6 polymorphisms
Patent: WO 0218638-A 1 07-MAR-2002;
Gemini Genomics PLC (GB)
Location/Qualifiers
1. 9432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytochrome P450 IID6 (CYP2D6) gene, complete cds. M3338 M3388 IIII81303 Cytochrome P450; cytochrome P4
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/note="G00-132-127"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
2647 c 2976 g 1845
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       AX394456
AX394456.1 GI:21065594
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/partial
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ORGANISM
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Direct Submission
Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND (1985) 1 to 13278)
Heim, M.H. and Meyer, U.A.
Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6
Genomics 14 (1), 49-58 (1992)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 13278)
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CYP2D7AP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens.
Homo sapiens.
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Human CYP2D7AP pseudogene for cytochrome P450 2D6
X58467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40.6; DB 9;
Pred. No. 4.4e-06;
1; Mismatches 0;
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/note="ACCCTTCCCC"
                                                                                                                                                4031. .4207
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4735. .4922
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               3356. .3443
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/gene="CYP2D7BP"
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/qene="CYP2D7BP"
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/gene="CYP2D7BP"
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/gene="CYP2D7BP"
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/gene="CYP2D7BP"
                                                           3444. .3605
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/gene="CYP2D7BP"
                                                                                                                                                                                               1208. .4399
/gene="CYP2D7BP"
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/gene="CYP2D7BP"
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97.6%;
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Eest Local Similarity 97.64
Matches 40; Conservative
    'number=3
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5377. .55
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Es Heim, M.H.

Direct Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre Chiversity of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND

Es Heim, M.H. and Meyer, U.A.

E (bases 1 to 13677)

E Heim, M.H. and Meyer, U.A.

Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6

LE Genomics 14 (1), 49-58 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(1534. .1801,2504. .2675,3203. .3355,3444. .3605,
4011. .4207,4400. .4540,4735. .4922,5377. .5518,5617. .5868)
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/gene="CYP2D7BP"
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HUMAN CYP2D7BP pseudogene for cytochrome P450 2D6.
X58468
X58468.1 GI:30337
CYP2D7BP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
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                                                                                                                                     Gaps
                                                                                                                                     0;
                                                                                                      Length 9432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See X58467, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
1. 13677
/organism="Homo sapiens"
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                                                                                                                                    0; Indels
                                                                                                                                                                Score 40.6; DB 9;
Pred. No. 4.7e-06;
1; Mismatches 0;
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                                                        2976 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
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                                                                                                      Query Match 99.0%;
Best Local Similarity 97.6%;
Matches 40; Conservative
                                           /number=9
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4031. .420
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PRI 21-OCT-1992

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JOURNAL Am. 7. Hum. Genet. 45 (6), 889-904 (1989)

MEDLINE 90072069

PUBBED 2574001

Draft entry and computer-readable sequence for [1] kindly submitted by S.Kimura, 29-MAR-1990.

Location/Qualifiers

Location/Qualifiers

Jordonism-"Homo sapiens"

Adb_Arefe^n" taxon:9606"

TATA_Signal 1276. 1282

prim_transcript 1304. 6570

/ Ooten"CYP2D8P mRNA and introns"

Join(1392. 1568, 3189. 3360, 3907. 4059, 4148. 4310, 4788. 4934, 5121. 2562,5467. 5651,6101. 6542,6339. 6516)
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                                                                                                                                                                                                                                    HUMCYP8P 17060 bp DNA 11near PRI 09-NOV-1994 Human debrisoguine 4-hydroxylase (CYP2D8P) and (CYP2D7) pseudogenes complete sequences.
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Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4 hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(1392, 11568, 3189, .3360, 3907, .4059, 4148, .4310, 4778, .4934, 5121, .5262, 5467, .5651, 6101, .6242, 6339, /gene="CYP20BP"
                                                                                             Gaps
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                                                            Length 13278;
                                                                                             1; Indels
                                                                                                                                                                                                                                                                                               M33387.1 GI:181320
debrisoquine 4 hydroxylase.
Human DNA, clones lambda-2D-A and lambda-2D-B.
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Best Local Similarity 95.1%; Pred. No. 2c-05;
Matches 39; Conservative 1; Mismatches
                 2744 t
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3664 c 3968 g 2744
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3651. .3827,4020. .4161,4356. .4542,4998. .5139,5238. .5489)
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1651. .3827,4020. .4161,4356. .4542,4998. .5139,5238. .5416)
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              See X58468, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
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                               FEATURES
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Laborited (22-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 25, 2001 this sequence version replaced gi:3204432.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw: SWISSPROT; Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMEPE database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                          PRI 22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr22
RPI-257120 is from the library RPCI-1 constructed by the group of
pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the entire insert of clone RP1-257120 The true right end of clone RP1-18601 is at 20171 in this sequence. Location/Qualifiers
Human DNA sequence from clone RP1-257120 on chromosome 22g13.1-13.2, complete sequence.
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      HS257120/c
                                            DEFINITION
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KEYWORDS
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15320. 11496)
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/evidence=not_experimental 9981. .10378

misc_feature

RESULT 9

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//Occe-march: 655: Em:AQ618257"
//Occe-march: 656: Em:AQ618257"
//Occe-march: 656: 703. 767 of consensus"
//Occe-march: 64357
//Occe-march: 64357
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//Occe-march: 658: Em:B13983"
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                                                                                                                        /notes | WIRT7 | repeat: matches 30. 587 of consensus | 58051. 59086 | /notes | 700 | 150086 | /notes | 700 | 150086 | /notes | 700 | /ootes 
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/note-"match: GSS: Em:AQ084812"
/note-"match: GSS: Em:AQ084812"
/note-"match: GSS: Em:AQ084812"
/note-"match: GSS: Em:AQ044403"
/note-"match: GSS: Em:AQ044403"
/note-"match: GSS: Em:AQ044403"
/note-"match: GF017
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/note-"match: GSS: Em:AQ044403"
54578. 55083 / mer ca 100% conserved" 54578. 55083 / notes"MER77 repeat: match
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//note-"11 copies 2 mer ac 100% conserved"
9274. .94444
/note-"Other . Weak data"
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104028. .104091
Anotes 2 copies 2 mer as 67% conserved"
complement(107923. .108378)
/notes match: GSS: Em:AQ572846"
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complement(78378 . 78961)
/note-"match: GSS: Em:AQ389013"
complement(78421 . 78533)
/note-"match: GSS: Em:AQ042556"
complement(78451 . 78977)
/note-"match: GSS: Em:AQ533248"
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/note="HERVI repeat: matches 2098. .2163 of consensus" 30902. .30971
/note="HERVI repeat: matches 2098. .2163 of consensus" 30961. .31556
/note="HERVI repeat: matches 1561. .2163 of consensus" 31873. .33456
/note="HERVI repeat: matches 9. .1561 of consensus" 33464. .33959
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27147. .28076
/note-"HERVI repeat: matches 4455. .5408 of consensus"
8886. .30853
/note-"HERVI repeat: matches 2098. .4455 of consensus"
10843. .30912
                                                                                             // Anotes | Marial | Topeat: matches | 1.1057 of consensus | 16086. 16507 | 16086. 16507 | 16086. 16507 | 16086. 16507 | 16086. 16507 | 17055. 17127 | 17055. 17127 | 17055. 17127 | 17056. 17127 | 17056. 17127 | 17056. 17127 | 17056. 17127 | 17056. 17127 | 17056. 17127 | 17056. 17127 | 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 17056. 170
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/noteu-LTR12 repeat: matches 5. .671 of consensus"
48150. .49467
/noteu-"CpG island"
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/note:"match: STS: Em:G43129"
43992. .44915
/note:"PTRS repeat: matches 40. .93 of consensus"
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20965. .20982
/note-"LIP repeat: matches 2294.
21270. .22130
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25597. 2608
700tes"match: GSS: Em:B13982"
25611. 25853
/notes"match: GSS: Em:B14069"
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/notes"match: GSS: Em:AF046780"
26890. 26995
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/notew"L1P repeat: matches 2416.
20246. .20284
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20594. .20660
                                           Em: AQ124532"
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13208. .14275
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Loh, P., Qi,S., Ford,B., Hine,R. and Roe,B.A.
Direct Submission
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Contact: humquery@sanger.ac.uk
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78.0%;
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Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek, A., Piepenbrock, C. and Berlin, K.
Method and nucleic acids for pharmacogenomic methylation analysis
Patent: WO 0202806-A 39 10-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 207709)
Loh, P., Qi,S., Ford, B., Hine, R. and Roe, B.A.
Mus musculus Chromosome 16 BAC Clone rp23-198m10
                                                                                                                  Uccall., 1884
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
92 c 1514 g 3019 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
/92 c 1514 g 3019 t
                                                                                                                                                                                                                                                                          Gaps
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                                           Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 529 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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0
                                                                                                                                                                                                                                         6; Length 5884;
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Pest Local Similarity 85.4%; Pred. No. 0.0088;

Matches 35; Conservative 1; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                       Score 32.6; DB 6;
Pred. No. 0.0088;
1; Mismatches
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Sequence 39 from Patent WO0202806
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  Location/Qualifiers
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2 (bases 1 to 207709)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic construct.
synthetic construct
artificial sequences.
                                                                                                                                                                                                                                      79.5%;
ilarity 85.4%;
Conservative
              artificial sequences
 synthetic construct
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Best Local Similarity
Matches 35; Conserv
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AC087799/c
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                               REFERENCE
                                              AUTHORS
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/clone="rp23-198m10"
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/note="This is one of two clones in well rp23-198m10"
4 46940 c 45622 g 58713 t 100 others
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Submitted (26-JAN-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA (bases 1 to 207709)
Loh, P., Qi,S., Frod, B., Hine, R. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                 Submitted (01-306-2002) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, 67 73019, USA.

On Jul 12, 2002 this sequence version replaced gi:21672179.

Center: Department Of Chemistry And Biochemistry
Center code:UOKNOR.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittuor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 60622: contig of 60622 bp in length
* 60623 60722: gap of unknown length
* 60723 207709: contig of 146987 bp in length.
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Pred. No. 0.48;
1; Mismatches 8; Indels 0;
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Center code: SC
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/chromosome="19"
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1. .207709
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HTG; HTGS_PHASE1.
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HTG 09-AUG-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 220770)
Ellington, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humqueryfsanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21911661.
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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/ fragment_chain:1"
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/ fragment_chain:1"
134915. .152680
/ note-"assembly_fragment:01654
/ fragment_chain:1"
152781. .167109
/ note-"assembly_fragment:00069
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                   /note="assembly_fragment:00083
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112537. .123477
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a 42820 c 41977 g 50956 t
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Contact: humquery@sanger.ac.uk
104630. .112436
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Best Local Similarity 79.5%;
Matches 31; Conservative
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AL772150/c
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                                                                               Chemistry Dye-terminator; 100% of reads
Consensus quality: 188691 bases at least Q40
Consensus quality: 189494 bases at least Q30
Consensus quality: 189925 bases at least Q30
Insert size: 190296; sum-of-contigs
Insert size: 19147; 5.6% error; agancse-fp
Quality coverage: 5.82x in Q20 bases; sum-of-contigs Quality
coverage: 6.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101593 101592: gap of 100 bp 101 tengum 101593 104529: contig of 2937 bp in length 104530 104629: gap of 100 bp 104629: gap of 100 bp 104639 104629: gap of 100 bp 104639 112537 12536: gap of 100 bp 112537 12536: gap of 100 bp 123478 123477: contig of 10341 bp in length 12357 123477: contig of 102 bp 123577: gap of 100 bp 134815 134814: contig of 11237 bp in length 134915 135280: contig of 11237 bp in length 155281 152780: contig of 100 bp 152781 167109: contig of 14329 bp in length 155781 167109: contig of 14329 bp in length 167210 186640: contig of 1431 bp in length 186741 186740: gap of 100 bp 186740: gap of 100 bp 186741 186740: gap of 100 bp 186741 186741 191496: contig of 4756 bp in length.
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77187 77286: gap of 100 bp
77287 101492: contrg of 24206 bp in length
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5235 13968: contig of 8734 bp in length
13969 14068: gap of 100 bp
14069 22628: contig of 8560 bp in length
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                                                                Assembly program: XGAP4; version 4.5
----- Project Information
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/clone="RP23-419B9"
                   Center project name: bM419B9
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* NOTE: This is a 'working draft' sequence. It currently

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consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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50486: contig of 45082 bp in length
50407 50586: gap of 100 bp
50587 62563: contig of 11977 bp in length
                                                                                                                                                                                                                                                                                                                                                          62564 62663: gap of 100 bp 62664 77675: contig of 15012 bp in length
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82568: contig of 2583 bp in length
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98148: contig of 3007 bp in length
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/note="assembly_fragment:02083
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5405 .50486
/note="assembly_fragment:01926
fragment_chain:1"
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fragment_chain:2"
5264. .77675
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fragment_chain:2"
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/note="assembly_fragment:00374"
86062. .88312
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/note="assembly_fragment:00210"
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/note="assembly_fragment:00025"
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/db_xref="taxon:10090"
/chromosome="4"
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alianzarunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Bencho, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunay, C., Burch, P., Burkett, C., Burell, K.L., Byrd, N.C., Carron, T.E., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davia, M.D., Dathorne, C., Earler, C., Edgaro, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan Rocha, S., Durbin, K.J., Earnbart, C., Edgar, D., Elagy, N., Ford, J., Escotto, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gorrell, J.H., Guevara, W., Ganreite, P., Hanle, S., Hamilton, K., Harts, K., Howard, S., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hollows, C., Howard, S., Huber, J., Hune, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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88413. .92031
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                                                     92132. .95041
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98249. .100384
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100485. .102543
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102644. 104695
/note="assembly_fragment:01706"
104796. 107219
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112022. .114336
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114437. . .131340
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/note="assembly_fragment:01180
fragment_chain:3
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Best Local Similarity 79.5%;
Matches 31; Conservative
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NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 160365)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 2, 2002 this sequence version replaced g1:21239896.

Center: Baylor College of Medicine
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Center close name: CH230-247A12
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Bly Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 87646 bases at least Q40
Consensus quality: 94706 bases at least Q30
Consensus quality: 94581 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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2: contig of 2319 bp in length
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2: contig of 1367 bp in length
2: contig of 1367 bp in length
3: contig of 1367 bp in length
3: contig of 2116 bp in length
3: contig of 2711 bp in length
3: gap of unknown length
3: contig of 2711 bp in length
3: gap of unknown length
4: gap of unknown length
4: gap of unknown length
5: contig of 3515 bp in length
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Best Local Similarity 78.9%;
Matches 30; Conservative
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Search completed: February 11, 2003, 05:33:25 Job time : 257.088 secs

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1 Similarity 70.0
28; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-103-840A-2
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US-09-103-840A-1
TYPE: DNA
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Sequence 10, Appli
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Sequence 1,
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US-09-024-020B-2
US-09-024-020B-7
US-09-425-043-7
US-09-024-020B-4
US-09-024-020B-4
US-09-024-020B-8
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US-09-103-840A-1
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US-08-814-052-19
US-08-814-052-17
US-08-814-052-18
US-08-939-218A-1
PCT-US95-06815-1
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US-08-646-715-4
US-08-318-831-1
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            version - 2003 (
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41
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Maximum Match 100%
Listing first 45 summaries
                                                               sw model
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Gapop 10.0 , Gapext 1.0
            GenCore
Copyright (c) 1993
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                                                            nucleic search, using
                                                                                      February 10, 2003,
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length: 2000000000
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Sequence 2, Aprilcation US/09103840A
Fatent No. 6294328
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPELICANT: FLEISCHUAN, Robert D.
APPLICANT: FRASE, Claire M.
APPLICANT: FRASE, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 4403765
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-220007.00
CURRENT RAPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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US-09-083-485-1
US-09-005-397-26
US-09-188-207A-28
US-09-188-930-273
US-09-188-930-261
US-09-188-930-261
US-09-579-181-11
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US-08-213-4198-20
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US-08-246-403A-7
US-08-246-403A-7
US-08-246-403A-7
US-08-246-403A-7
US-08-246-403A-10
US-08-246-403A-7
US-08-246-403A-10
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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CURRENT APPLICATION DATA:
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Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: FISH, LINDA M.
APPLICANT: SANGAMESWARSANA, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Michael, Jennifer L.
APPLICANT: Michael, Jennifer L.
APPLICANT: Ming, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN:
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.46662
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                     Indels
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Pred. No. 27;
0; Mismatches 12;
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                                                                                                                                                           Score 22; DB 4
Pred. No. 37;
1; Mismatches
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3401 HILLVIEW AVENUE, MS A2-250
                                                        TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                         Sequence 223, Application US/09397787
Patent No. 6468758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 70.7%;
Matches 29; Conservative (
                                                                                                                                                         53.7%;
ilarity 70.0%;
Conservative
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SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
US-09-397-787-223
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COUNTRY: U.S.A.
"TP: 94304-1397
                                                                                                                                                       Query Match
Best Local Similarity
Matches 28; Conserv
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STREET: 3401 HII
CITY: PALO ALTO
                                     4411529
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US-09-024-020B-1/c
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                                       LENGIH:
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Sequence 1, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DESCADO, STEPHEN G.
APPLICANT: DISTRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SOUTOM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF NUMBER OF SEQUENCES: 43
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APPLICATION NUMBER: US/09/425,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cuery Match 52.2%; Score 21.4; Di
Best Local Similarity 68.3%; Pred. No. 48;
Matches 28; Conservative 1; Mismatches
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STREET: 3401 HILLVIEW AVENUE, MS A2-250
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSITCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY FAGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
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SOFTWARE: Patentin Release #1 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: DNA (genomic) US-09-024-020B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: ('
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US-09-425-043-2/c
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Petent No. 6030810
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DIETRICH, PAUL S.
APPLICANT: HERMAN, RONALD C.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWAREN LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,799
ER: R0020B-REG
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                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.2%;
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6007 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                         Query Match 52.2
Best Local Similarity 68.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.2
Best Local Similarity 68.3
Matches 28; Conservative
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2825 AGGAAGGAGTGGAAGAAGTCGTTCATGTGCCAGCGCGGAG 2785

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GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: FISH, LINDA M.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                             APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21.4; DE Pred. No. 48; 1; Mismatches
                                                                                                                                                                                                                                                                           E: JANET PAULINE CLARK
3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY,AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R020B-REG
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/09024020B
; Patent No. 6030810
Sequence 2, Application US/09425043; Patent No. 6335172; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                     APPLICANT: DELGADO, STEPHEN G. APPLICANT: DIETRICH, PAUL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.2%;
68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6007 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 68.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                           PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-024-020B-7/C
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                                                                                                                                                                                                                                                                                                                                                STATE:
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PALO ALTO
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US-09-024-020B-43/c
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APPLICANT: DIETRICH, PAUL S.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARMAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SOUTOM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2942 AGGAAGAGTGGAAGAAGTCGTTCATGTGCCAGCGGGGAG 2902
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B FILLIG DATE: 16 FFBB-1998 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin & DOJ/HO DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/425,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULLINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21.4;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CLARK, JANET P.
REGISTRATION UNDRER: 34,799
REFRENCE/DOCKET UNDRER: R002(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFRAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09425043
Patent No. 6335172
                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.2%;
68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 6556 base pairs
                                                                                                     STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DELGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 94304-1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-425-043-7/C
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STATE:
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GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: PISH, LINDA M.
APPLICANT: APRLICANT: APRLICANT: TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
OFFWARE: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PATE:
APPLICATION NUMBER: US/09/024,020B
FLILNG DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 60/039,447
FILING DATE: G-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JAMET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
MARE: CLARK, JAMET P.
REGISTRANCE/POCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
MATERIALING PROPAGATION INFORMATION:
METERERENCE/POCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
METERERENCE/POCKET NUMBER: R0020B-REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2942 AGGAAGGAGGAAGAAGTCGTTCATGTGCCAGCGCGGAG 2902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.4; DI
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                         NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 43, Application US/09024020B
; Patent No. 6030810
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-425-043-7
                                                                                                                                                                                                                                                                   TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%;
                                                     FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 6(
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 6556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6586 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.29
Best Local Similarity 68.39
Matches 28; Conservative
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6826 base pairs
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LENGTH: 6826 base pair
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EDNESS: single
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Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: FISH, LINDA M.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEROF
INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEROF
INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEROF
INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEROF
INVENTESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
IP: 94304-1397
COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-0SS/MS-DOS
SOFTWARE: PALCATION DATA:
APPLICATION NUMBER: US/09/425,043
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                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                   2972 AGGAAGGAGTGGAAGAAGTCGTTCATGTGCCAGCGCGGGAG 2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.2%; Score 21.4; DB 3; 18est Local Similarity 68.3%; Pred. No. 48; Matches 28; Conservative 1; Mismatches 12;
                                                                                                                                                                                                                     1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.2%; Score 21.4; DB 4; ilarity 68.3%; Pred. No. 48; Conservative 1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R0020B-REG
                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/09425043 Patent No. 6335172 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: RC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 6586 base pairs
                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-024-020B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     US-09-425-043-43/C
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RESULT 13
US-09-425-043-8/C
Sequence 8, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: APPLICANT: AND M.
APPLICANT: APPLICANT: AND M.
APPLICANT: APPLICANT: AND M.
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
US-09-024-020B-8/c
Sequence 8, Application US/09024020B
Sequence 8 Application US/09024020B
Sequence 8 Application
Sequence 8 Application
Sequence 8 Application
Sequence 8 Applicant
Sequence 8 Applicant
Sequence 8 Applicant
Sequence 8 Applicant
Sequence 9 STEPHEN G.
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: FISH, LINDA M.
APPLICANT: FISH, LINDA M.
APPLICANT: SANGAWESWARNN, LAKSHMI
APPLICANT: SANGAWESWARNN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SOUTUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION NUMBER: US 60/039,447
FILING APPLICATION DATA:

APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INMBER: R0020B-REG
TELECOMMUNICATION INMBER: R0020B-REG
TELEPHONE: (650) 855-5322
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2768 AGGAAGGAGTGGAAGAAGTCGTTCATGTGCCAGCGCGGGAG 2728
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                                                                                                                                                                                                                                                                                                                                                                                                           E: JANET PAULINE CLARK
3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.2%; Score 21.4; 68.3%; Pred. No. 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TAN PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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A-57650-2/AJT/RAO

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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION UNDRER: 36,627
REFERENCE/DOCKET UNDRER: A-57(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
IFLER: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 26, Conserv
                                                 FILING DATE: 28
CLASSIFICATION:
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LOCATION:
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US-08-646-715-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-188-582-4
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APPLICANT: Tjian, Robert
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hopy, Timothy
APPLICANT: Tanese, Nacko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2768 AGGAAGGAGGAAGAAGTCGTTCATGTGCCAGCGCGGAG 2728
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

PREDICATION NUMBER: US 09/024,020

FILING DATE: 16-FEB-1998

APPLICATION NUMBER: US 60/039,447

FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799

REFERNCE/DOCKET NUMBER: R0020B-REG

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R0020B-REG
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/425,043
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5534410
GENERAL INFORMATION:
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EDNESS: single
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Best Local Similarity
Matches 28; Conserv
                                  PALO ALTO
                                                                                                      COUNTRY: U.S.A. ZIP: 94304-1397
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Gaps
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APPLICANT: Comai, Lucio
APPLICANT: Comai, Lucio
APPLICANT: Pinothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Nacko
APPLICANT: Wang, Edith
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                       ·
0
                                                                                                                                                        Length 2359;
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION 435
PROR APPLICATION 1435
PROR APPLICATION 1985
FILING DATE: 28-JAN-1994
                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                          927 ACCAGAGGAGGACGATGATCCGGATGCCCGGGA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO IELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                            5 AGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGA 40
                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                        51.7%; Score 21.2; 72.2%; Pred. No. 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTOKNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
GAPPLICANT: Tjian, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 781-1989
                                                                                                                                                                                                    Conservative
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CITY: San Francisco
STATE: California
                                                                                       49..2160
TOPOLOGY: linear MOLECULE TYPE: CDNA
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Query Match 51.7%; Score 21.2; DB 1; Length 2359; Best Local Similarity 72.2%; Pred. No. 51; Matches 26; Conservative 1; Mismatches 9; Indels 0.
TELEFAX: (415) 398-3249
TELEX: 910 277299
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE:
NAME/KEY: CDS
US-08-646-715-4
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Gaps ó;

Search completed: February 11, 2003, 05:59:51 Job time : 1049.12 secs

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                                                                                                                     February 11, 2003, 03:31:30 ; Search time 3.72137 Seconds (without alignments) 5222.300 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                        1 agaaagcagtggaggaggac......accctcaggcagccgggag 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
version 5.1.3
- 2003 Compugen Ltd.
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US-09-789-404-1

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US-09-864-761-19007

US-09-864-761-2269

US-09-864-761-2269

US-09-864-761-2269

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US-09-880-107-3949
US-09-923-876-460
US-09-835-232-7
US-09-822-849A-95
US-09-864-761-26896
                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           408267 seqs, 237001491 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                     US-09-942-310-2_COPY_600_640
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Maximum Match 100%
Listing first 45 summaries.
                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                                                           IDENTITY_NUC Gaport 1.0
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
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66:
77:
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Maximum DB seq
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Perfect score:
                                                                                                                                                                                                                                                                                               Scoring table:
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David K.
APPLICANT: Hank, David K.
APPLICANT: Hank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HANK GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: HANK GENOME-A-1
CURRENT FILING DATE: 2001-65-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR PLILNG DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: US 60/203,366
PRIOR FILING DATE: 2000-05-20
PRIOR PPLICATION NUMBER: US 60/203,366
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
                                               sequence 1652, Ap
Sequence 1652, Ap
Sequence 11, Appl
Sequence 11, Appl
Sequence 2188, Ap
Sequence 2036, Ap
Sequence 2036, Ap
Sequence 1986, Ap
Sequence 2036, Ap
Sequence 2139, Ap
Sequence 2195, Appl
Sequence 1, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1475, Ap
Sequence 1364, Ap
Sequence 839, App
Sequence 3565, Ap
0 US-09-998-598-1948

0 US-09-864-761.10261

0 US-09-864-761.10261

0 US-09-777-564-1652

0 US-09-777-564-1652

0 US-09-777-564-1652

0 US-09-788-65-2188

US-10-046-935-1986

US-10-046-935-2036

US-09-788-656-2188

US-09-788-656-2188

US-09-788-656-2188

US-09-788-656-2188

US-09-788-686-595

US-09-788-686-595

US-09-784-888-5

US-09-884-71118234

US-09-884-761-18234

US-09-884-761-18234

US-09-884-761-18234

US-09-884-761-18234

US-09-884-761-18234

US-09-884-761-18234

US-09-884-761-18234
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Patent No. US20020048763A1
    461
4428
341
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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL LEUCINE RICH REPEAT-CONTAINING MOLECULES AND USES THEREF
FILE REPERENCE: 10448/008001
CURRENT APPLICATION NUMBER: US/09/789,404
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/456,592
PRIOR FILING DATE: 1999-12-08
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Pred. No. 3.3;
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                                               PRIOR PALLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTHARE: Annomax Sequence Listing Engine v
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Pred. No. 3.
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SOFTWARE: FastSEQ for Windows Version 4.0
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; NAME/KEY: misc_feature
; LOCATION: (1)...(2636)
; OTHER INFORMATION: n = A,T,C or US-09-789-404-1
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73.2%;
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73.2%;
                         FILING DATE: 2001-01-30
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Best Local Similarity 73.2%
Matches 30; Conservative
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Best Local Similarity 73.2 Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MOTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
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LOCATION: (33)
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US-09-789-404-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 9308
LENGTH: 555
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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EST_HUMAN HIT: BF448000.1, EVALUE 2.00e-84
SWISSPROT HIT: P16356, EVALUE 2.00e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
N: EXPRESSED IN BARIN, SIGNAL = 3
N: EXPRESSED IN PLACENTA, SIGNAL = 1.8
N: EXPRESSED IN HERA, SIGNAL = 3.3
N: EXPRESSED IN HERAT, SIGNAL = 1.9
N: EXPRESSED IN LUNG, SIGNAL = 3.3
N: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3
N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Pred. No. 2.9;
1; Mismatches
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PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR PELING DATE: 2000-08-03
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00668
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP TO ALU
EXPRESSED
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73.2%;
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Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-864-761-25857
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US-09-864-761-9308
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 25857
LENGTH: 159
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Gaps

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Indels

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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown Organism: Chp, EMBL No. US20020150971A1 OTHER INFORMATION: 9921y0
                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 10; Length 1845; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1504 GACAGCTGTGGAGAAGGCCGACACCTGGGCTGCCTCGAG 1543
                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00669
PRIOR PELICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234, 687
PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR PILING DATE: 2001-01-30
CURRENT APPLICATION NUMBER: US/09/778,844
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 206
SEQ ID NO 64
LENGTH: 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 18173, Application US/09864761
; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                    53.78;
70.08;
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                        ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.0
Matches 28; Conservative
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US-09-864-761-18173
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                                                                                                                                                                 TYPE: DNA
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APPLICANT: SCHALLING, MARTIN
TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES FOR CONTROLLING FOOD
TITLE OF INVENTION: INTRAKE AND/OR BODY WEIGHT
FILE REFERENCE: 030307/0195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEO ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                   Sequence 490, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
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DB 10;
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Best Local Similarity 76.5%; Pred. No. 23;
Matches 26; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME, KEY: SITE
LOCATION: (116)
OTHER INFORMATION: n equals a,t,g, or
NAME, KEY: SITE
LOCATION: (244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (394)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (305)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: SITE
LOCATION: (3305)
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Patent No. US20020150971A1
GENERAL INFORMATION:
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FEATURE:
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LOCATION: (448)
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                                                                                                    RESULT 4
US-09-764-864-490
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LENGTH: 3314
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US-09-778-844-64
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OTHER INFORMATION: EXPRESSED IN HELLIOO, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN HELLIOO, SIGNAL = 8.4

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 5

OTHER INFORMATION: EXPRESSED IN FIRTAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN PICTAL LIVER, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0

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OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0

OTHER INFORMATION: EXPRESSED IN BY 474, SIGNAL = 3.0
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APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: COMPOSITIONS AND METHODS FOR CVARIAN FILLE OF INVENTION NUMBER: US/09/876,889
                                          PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-30

PRIOR FILING DATE: 2000-06-30

PRIOR PILICATION NUMBER: US 09/774,203

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 1907
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Pred. No. 31;
0; Mismatches
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Pred. No. 29
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SOFTWARE: FastSEQ for Windows Version 3.0
                APPLICATION NUMBER: PCT/US01/00670
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Matches 29; Conservative
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Best Local Similarity 70.7°
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-09-876-889-223
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US-09-864-761-2269/c
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US-09-876-889-223
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
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EST_HUMAN HIT: AI281103.1, EVALUE 1.00e-106
SWISSPROT HIT: P30711, EVALUE 5.00e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 195;
                                                                                                                                                                                                                                                                              N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
N: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4
N: EXPRESSED IN PLACENTA, SIGNAL = 1.8
N: EXPRESSED IN HELA, SIGNAL = 2
N: EXPRESSED IN HEART, SIGNAL = 3
N: EXPRESSED IN HEART, SIGNAL = 7.2
N: EXPRESSED IN HEALOO, SIGNAL = 7.2
N: EXPRESSED IN BRAIN, SIGNAL = 1.9
N: EXPRESSED IN LUNG, SIGNAL = 1.9
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 18173
LENGTH: 195
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Pred. No. 29;
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR PLICATION NUMBER: US 02/632,366
PRIOR PLILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
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PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                    TO Z84718.2
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Best Local Similarity 70.7%;
Matches 29; Conservative
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                                                                                                                                                                ORGANISM: Homo sapiens
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INFORMATION:
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-09-864-761-19007/c
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N: MAP TO 284718.2
N: EXPRESSED IN FETAL LIVER, SIGNAL "1.5
N: EXPRESSED IN ADULT LIVER, SIGNAL "3.4
N: EXPRESSED IN HELA, SIGNAL "1.8
N: EXPRESSED IN HERA, SIGNAL "2.4
N: EXPRESSED IN HERAT, SIGNAL "2.6
N: EXPRESSED IN HEART, SIGNAL "2.6
N: EXPRESSED IN HEART, SIGNAL "7.2
N: EXPRESSED IN BRAIN, SIGNAL "1.9
N: EXPRESSED IN BRAIN, SIGNAL "1.9
N: EXPRESSED IN BONE MARROW, SIGNAL "1.1
        RESULT 10
US-09-864-761-2795
; Sequence 2795, Application US/09864761
; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-09-864-761-2795
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INFORMATION:
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INFORMATION:
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                                                           APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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NE EXPRESSED IN LUNG, SIGNAL = 5

NE EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

NE EXPRESSED IN PACENTA, SIGNAL = 4.3

NE EXPRESSED IN PLACENTA, SIGNAL = 7.3

NE EXPRESSED IN HELA, SIGNAL = 7.3

NE EXPRESSED IN BRAIN, SIGNAL = 2.9

NE EXPRESSED IN BRAIN, SIGNAL = 2.9

NE EXPRESSED IN BRAIN, SIGNAL = 3.9

NE EXPRESSED IN BYA74, SIGNAL = 12
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR ELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 2269
LENGTH: 461
                                                                                                                                                                                   TILE REFERENCE: AGOMICAS X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-09-07

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-04

PRIOR PLING DATE: 2001-01-03

PRIOR PLING DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR DATE: 2001-01-30
Sequence 2269, Application US/09864761
Patent No. US20020048763A1
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Best Local Similarity 70.7%;
Matches 29; Conservative
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1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-22
                                                                                                                                           Query Match
Best Local Similarity
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US-09-764-860-1102/c
LOCATION: (627)
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LENGTH: 17252
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                     DB 10; Length 462;
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## GENERAL INFORMATION:
## APPLICANT: Rosen et al.
## TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
## FILE REFERENCE: PA105
## CURRENT APPLICATION NUMBER: US/09/925,297
## CURRENT FILING DATE: 2001-08-10
## PRIOR APPLICATION NUMBER: PCT/USO0/05989
## PRIOR APPLICATION NUMBER: PCT/USO0/05989
## PRIOR FILING DATE: 1999-03-12
## NUMBER OF SEQ ID NOS: 928
## SOFTWARE: Patentin Ver. 2.0
## SEQ ID NO 306
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPERENCE: PALOS

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2009-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: PatentIn Ver. 2.0
                                                              Indels
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                                                                                                                            53.2%; Score 21.8; DB 10;
70.7%; Pred. No. 32;
Live 0; Mismatches 12;
        53.2%; Score 70.78; Pred. No. 32; 70.7%; Pred. No. 32; 70.7%; Msmatches 12; 74.7%
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                                                                                                      1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
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LOCATION: (584)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
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CATION: (620)

CATHORNATION: n equals a,t,g, or c

US-09-925-297-303
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                                                                                                                                                                                                                                                  Sequence 303, Application US/09925297 Patent No. US20020081659A1
                                      Best Local Similarity 70.7
Matches 29; Conservative
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Matches 29; Conservative
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US-09-925-297-303
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LENGTH: 620
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                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A
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                                                                                                                       DB 10; Length 906;
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Sequence 1102, Application US/09764860

SENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008

FILE REFERENCE: PC008

CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCGGGAG 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21.8; DE Pred. No. 45; 0; Mismatches
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
PRIOR APPLICATION NUMBER: 60/298,309
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAG 33
                                                                                                                     Score 21.8;
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                                        ; LOCATION: (863)
; OTHER INFORMATION: n equals a,t,g,
US-09-925-297-302
                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09964899 Patent No. US20020174446A1
                                                                                                                     53.28;
70.78;
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Best Local Similarity 70.7%;
Matches 29; Conservative
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Best Local Similarity 78.8'
Matches 26; Conservative
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                   NAME/KEY: misc feature LOCATION: (863)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-764-860-1102
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Db 11693 AGAAAACTGTGGAGGAGGAACACCCGGAGGGAG 11661

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RESULT 15
US-09-880-107-3949
Sequence 3949 Application US/0980107
Sequence 3949 Application US/0980107
Sequence 3949 Application US/0980107
SERNEAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Gene Logic, Inc.
TITLE OF INVERTION: Gene Logic, Inc.
TITLE OF INVERTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT FILING DATE: 2001-06-14
FRIOR APPLICATION NUMBER: US 60/211,379
FRIOR APPLICATION NUMBER: US 60/211,379
FRIOR APPLICATION NUMBER: US 60/237,054
FRIOR APPLICATION NOW SET 200-6-14
SOFTWARE: PatentIN Ver. 2.1
FYPE: DNA
OCHER INFORMATION: Genbank Accession No. US20020142981A1 284718
OCHER INFORMATION: Genbank Accession No. 52;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps
OV 1 AGAAAGCAGTGGAGGAGCACCCCATGAG 15575

OUG 15535 AGGCAGCAGCACCACTTCTCCAGGAGCCCATGAG 15575
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Search completed: February 11, 2003, 09:09:13 Job time : 12.7214 secs

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Human secreted exp Human H83-22 secre 5' fragment of elo Human prostate exp Stomach cancer rel

Human ORFX polynuc Human secreted pro

Human H83-22 secre Human hPEPT1 gene Human reproductive Human box-dependen Human Bin1 gene. Partial human geno

Perfect score:

Run on:

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Scoring table:

Minimum DB s Maximum DB s

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Result

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Cytochrome P450; CYP2D6; promoter; drug metabolism; human; diagnosis; therapy; ds.
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complement (14..36)
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complement (565..577)
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/note= "sequencing primer R3"
complement (968..988)
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ABS02512
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ABV09249
ABV39400
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ABL26934
         AAC22210
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AAA43852
AAT91307
AAV00431
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ABL64398
AAT91308
AAH26535
AAL04162
AAL1652
AAV15693
AAX16323
ABA43852
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AAK28030
AAI12612
AAI33964
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ABA24072
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 17-SEP-2001 (first entry)
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                                                             February 10, 2003, 20:43:59; Search time 16.6596 Seconds (without alignments) 5542.256 Million cell updates/sec
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N. Leoneseg_101001:

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11: SIDS2/gcgdata/geneseg/genesegn-embl/NA1981.DAT:*

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24: SIDS2/gcgdata/geneseg-genesegn-embl/NA2001.DAT:*
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Compugen Ltd.
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                                                                                                                                                                  2185239 segs, 1125999159 residues
         GenCore version
Copyright (c) 1993 - 2003
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41
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Maximum Match 100%
Listing first 45 summaries
                                            OM nucleic - nucleic search, using sw model
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AAH26179
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AAD34213
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ABL32556
ABA20740
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Human genome-derlv
Human prostate exp
Human prostate exp
Human prostate exp

Human reproductive Human polynucleoti Human nervous syst

Arabidopsis thalla Arabidopsis thalla Drosophila melanog Human ovarian canc

Human prostate exp Genomic sequence #

0;

Gaps

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Indels

Length 1669;

Score 40.6; DB 22; Pred. No. 5.2e-07; Mismatches

99.0%; Scor 100.0%; Pre 0;

Query Match
Best Local Similarity 100.
Matches 41; Conservative

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5'UTR
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The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene. The promoter region was amplified by PCR from leucocyte DNA of over 50 individuals, and sequenced. By PCR from leucocyte DNA of over 50 individuals, and sequenced. PCR from leucocyte DNA of over 50 individuals, and sequenced. PCR from leucocyte DNA of over 50 individuals, and sequenced. CC identified. These were at: base 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature), where the SNP was C to CC dunction and restimated frequency of approximately 20% in the population, and resulting in increased enzyme activity. CC CC function; position 385 (-1235), A to G, approximately 20% frequency, neutral function; position 620 (-1000), G to A, approximately 30% frequency, unknown function; position 940 (-680), CC approximately 30% frequency, unknown function; 1255 (-365), CC approximately 30% frequency, unknown function; 1255 (-365), CC G to A, approximately 30% frequency, unknown function; 1255 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, unknown function; 256 (-365), CC G to A, approximately 30% frequency, u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide capable of hybridizing to CYP2D6 promoter useful for se optimization of drug therapies using substrates of cytochrome P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on in vivo drug metabolism capacity, thus providing a very pote tool for improving the therapy of diseases with drugs that are targets of the CYP2D6 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "5' region of CYP2D6 coding region"
                                                                                                                                                                                                                                                                                                                                                         'note= "amplification primer upr1669"
                                                                                                                                R4 "
"sequencing primer F3"
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note= "sequencing primer
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"sequencing primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 41pp; English.
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/note= "sec
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.620..1669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-457734/49.
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Sequence 1669 BP; 413 A; 376 C; 534 G; 338 T; 8 other;
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A polynucleotide capable of hybridizing to CYP2D6 promoter useful for the optimization of drug therapies using substrates of cytochrome P-450
                                                                                                                               Human cytochrome P450 CYP2D6 gene promoter (G mutation at -1584 bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonist, tricyclic antidepressant, selective serotonin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a muttation in the CYP2D6 promoter. The novel variant forms of the CYP2D6 gene provided by the invention provide the potential for the development of a pharmacodynamic profile of drugs for a given patient. The finding and characterization of variations in the CYP2D6 gene, and diagnostic tests for the discrimination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene, which includes G at position 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature). The presence of C at position -1584 bp is a marker for low enzyme activity, whereas there is strong association of G at position -1584 bp with increased enzyme activity. The C to G single nucleotide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates (antiarrhythmic, beta adrenergic receptor
                                                                                                                                                                   human;
                                                                                                                                                                                                                                                                                                                                                                                                /note= "5' region of CYP2D6 coding region"
                                                                                                                                                              Cytochrome P450; CYP2D6; promoter; drug metabolism; diagnosis; therapy; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1(a); Page -; 41pp; English.
                                                                                                                                                                                                                                                                                                /frequency= "20%"
1532..1619
                              AAH26179 standard; DNA; 1669 BP.
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different alleles in human individuals, provide a very potent tool for improving the therapy of diseases with drugs that are targets of the CYP2D6 gene production, and whose metabolism is therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xenobiotic;
chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New sequence determination oligonucleotides, useful for detecting
                                                dependent on CYP2D6 activity.

Note: The present sequence is not shown in the specification but derived from the CYP2D6 promoter sequence given in the Sequence Listing (see AAH26169).
                                                                                                                                                                          / Match 99.0%; Score 40.6; DB 22; Length 1669; Local Similarity 100.0%; Pred. No. 5.2e-07; nes 41; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytochrome P450 2D6; CYP2D6; enzyme; detection;
ligase-based sequenced determination; drug metabolism;
                                                                                                                                            Sequence 1669 BP; 413 A; 376 C; 535 G; 338 T; 7 other;
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'note⊔ "Polymorphic site"
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"Polymorphic site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            AAD34214 standard; DNA; 1680 BP
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                                                                                                                                                                                                                                                                                                                                                                                                               AAD34214;
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                                                                                                                                                                                                Best Local
Matches
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                                                                                                                                                                                                                                                                                                                                         RESULT 3
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                                                                                                                                                                  The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase; antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertonsion; tricyclic antidpersessant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotyping; genotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ds.
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given as S in the specification"
replace (776, G)
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A)
polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYP2D6 gene 5' flanking region containing polymorphic sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1680 BP; 413 A; 379 C; 539 G; 342 T; 7 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.6; DB 24.
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Conservative 0; Mismatches
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replace (678,
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                                                                                                                    Claim 1; Fig 2; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ72215 standard; DNA; 6472
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/labela PS4
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/label- PS1
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/label⊳ PS2
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/label~ PS3
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/label~ PS5
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Matches 41; Conserv
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/*tag= u
//abel= PS17
/note= "Novel single nucleotide polymorphism (SNP);
ylote= "Novel single nucleotide polymorphism (SNP);
with PS18 causes the amino acid substitution
T107F"
                                                                                                                                                                                                                                                                                                                                                                   /note= "Novel single nucleotide polymorphism (SNP);
given as Y in the specification; together
with PS17 causes the amino acid substitution
T107F"
              /note= "Novel single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution V104A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution 1109V" replace (2036, C)
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given as Y in the specification"
replace (2039, T)
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given as W in the specification; causes the
amino acid substitution F1201"
replace (2635, C)
/*tag= ah
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given as R in the specification"
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given as S in the specification"
2606..2758
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given as R in the specification"
replace (2179, C)
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/cons_splice= (5'site:NO, 3'site:YES)
replace (2062, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace (2028, G)
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(2067, G)
                                                                                                (2022, T)
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/label= PS20
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/label= PS21
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/label= PS22
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/label= PS25
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/label= PS26
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/label= PS24
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/label= PS27
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              /*tag= k
/label= psg
/note= TROWN single nucleotide polymorphism (SNP);
given as Y in the specification; causes the
amino acid substitution P34S"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Known single nucleotide polymorphism (SNP);
given as R in the specification; causes the
amino acid substitution V7M"
/note= "Known single nucleotide polymorphism (SNP);
given as R in the specification"
                                                                                                                                     Novel single nucleotide polymorphism (SNP); given as Y in the specification" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right)
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given as R in the specification; causes the
amino acid substitution V11M"
replace (1100, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                //note= "Novel single nucleotide polymorphism (SNP);
    given as S in the specification"
replace (1843, G)
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/label= PS12
/note= "Novel single nucleotide polymorphism (SNP);
given as R in the specification; causes the amino acid substitution R88H"
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given as S in the specification"
                                                                                                                                                                                                                                               "CYP2D6"
                                                                                                                                                                                                                                                                                                                                                                 A)
                                  given as
(915, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1031, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace (1827, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace (1966, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1974, A)
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/label= PS10
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/label= PS15
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/label= pS16
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/note= "Novel single nucleotide polymorphism (SNP);
replace (1997, G)
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/label= PS9
/note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution P34S"
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/label- PS10
/note= "Novel single nucleotide polymorphism (SNP)"
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causes the amino acid substitution R88H"
replace (1974, A)
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/note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution L91M"
replace (1984, G)
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causes the amino acid substitution V104A"
replace (2022, T)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Novel single nucleotide polymorphism (SNP); together with PS17 causes the amino acid substitution T107F" replace (2028, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution I109V" replace (2036, C)
                                          /note- "Known single nucleotide polymorphism (SNP); causes the amino acid substitution V7M" replace (1031, A)
                                                                                                             /note- "Known single nucleotide polymorphism (SNP); causes the amino acid substitution V11M" replace (1100, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /labels PS15
/notes "Novel single nucleotide polymorphism (SNP)"
replace (2014, C)
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    à
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/label: PS17
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                                                                 /tega ai
/label= PS29
/note= "Novel single nucleotide polymorphism (SNP);
yiven as R in the specification; together
with PS30 causes the amino acid substitution
V1361"
                                                                                                                                                                                                                Gaps
              "Novel single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution W128R" (2659, A)
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replace (776, G)
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                                                                                                                                                                                99.0%; Score 40.6; DB 24; Length 6472;
llarity 97.6%; Pred. No. 7.1e-07;
Conservative 1; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human CYP2D6 gene, SEQ ID NO:1 version #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/label= PS28
/note= "Novel
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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobictics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in sprobes in sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic; ligase-based sequenced determination; drug metabolism; chromosome 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New sequence determination oligonucleotides, useful for detecting polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination
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                                                                                                                                                                                        241 GTGTGAGAGAATGTGTGCCCTAAGTGTCAGTGTGAGTCT 281
                                                                                                       Score 40.6; DB 24;
Pred. No. 7.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450 2D6 (CYP2D6) gene.
                                                                          replace (3292, A)
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          /number= 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                        variation
                                                                                                                                                                                                                                                                                                                       AAD34213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ds.
                                                                                                         Query Match
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Best Local 9
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                                                                                                                                                                                                                                                      RESULT 6
AAD34213
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        FT
                                                                                                                                                                        δ
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                                                                                                                                                                            The PS22 /note= "Novel single nucleotide polymorphism (SNP)" replace (2067, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution F1201"
replace (2635, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Known single nucleotide polymorphism (SNP)"
2847..3007
/*tag= ao
'note= "Novel single nucleotide polymorphism (SNP)"
                                                              /note= "Known single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                  /note= "Novel single nucleotide polymorphism (SNP)"
replace (2118, T)
                                                                                                                                                                                                                                                                                                                 /label= PS24
/note= "Novel single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Novel single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution W128R"
replace (2659, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Novel single nucleotide polymorphism (SNP); together with PS30 causes the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Known single nucleotide polymorphism (SNP);
together with PS29 causes the amino acid
substitution V1361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= PS32
/note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution E155K"
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                                                                                                                                                                                                                                                                                                                                                                                                /note= "Known single nucleotide polymorphism (SNP)
                                                                                                                                  /cons_splice= (5'site:NO, 3'site:YES) replace (2062, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substitution V1361"
(2661, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace (2611, A)
                                                                                                                                                                                                                                                                                                                                                                                                                    replace (2179, C)
                    replace (2039, T)
                                                                                                                                                                                                                                                                                                                                                   (2170, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace (2716, A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace (2846,
                                                label= PS21
                                                                                                                                                                                                                                                    /label= PS23
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/label= PS26
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/label= PS29
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/label= PS30
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4241 GTGTGAGAGAGAATGTGTGTTTTGAGTGTTAGTGTGAGTTT 4281

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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM_000693), CYPILA (NM_00091), CYPIB1 (NM_000497), CYP343 (NM_000776 and NM_017460), DPYD (NM_00190), CYPIB1 (NM_001999), CYPIRD1 (NM_001990), NM_019900, NM_019900, NM_019902, NM_019902, NM_019903, NM_019903,
                                                                                                                                                                                                                                                        Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP1181; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid, oligonuclectides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.5%; Score 32.6; DB 24; Length 5884; 85.4%; Pred. No. 0.0013; 1ve 1; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the printed specification, but was obtained in electronic mat directly from WIPO at
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                                                                                                                                                                                                               Human chemically pretreated gene sequence #20 strand 1.
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                                                 ABK39958 standard; DNA; 5884 BP
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                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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RESULT 7
                        ABK39958
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mycloid leukaemia, Alzheimer's disease, Allb., epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antiartiosclectuic antianaemic; cytostatic; mootropic; neuroprotective; antianaemic; cytostatic; mootropic; antisheumatic; antiarthritic; antidiabetic; antipsoriatic; antisheumatic; antiarthritic; antidiabetic; antipsoriatic; antisheumatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilopsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 529; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 529.
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                                  ABL32556 standard; DNA; 5884
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01-SEP-2000; 2000DE-1043826
                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytosine methylation
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Matches 35; Conserv
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RESULT 8
ABL32556
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Conservative

Best_Local Similarity Matches 35; Conserv

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2000US-0233063
2000US-0233064
2000US-0234223
2000US-0234274
2000US-0234997
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20000S-0251160.
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2000US-0249218
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14-SEP-2000; 2
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17-NOV-2000;
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17-NOV-2000;
        Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 Human nervous system related polynucleotide SEQ ID NO 13071
                                                                                                                                                                                                                                                                                    2000US-0179065.
2000US-0186628.
2000US-0184664.
2000US-0186350.
2000US-019874.
2000US-0198074.
2000US-0198123.
2000US-029467.
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2000US-0216647.
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2000US-0226688
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2000US-0232080.
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2000US-0218290.
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19-MAY-2000;
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AAC22210
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                                                                                                                                                                                                                                                                                             The Invention Letters to inver yenes (ABB14678-ABB18001) useful for preventing treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmonytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neerological diseases e.g. carebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal neers the sequence data for this patent did not form part of the printing specification, but was obtained in electronic format directly
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                                                                                                                                                                                                      Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                       The invention relates to novel genes (ABA11004-ABA21534) and proteins
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                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 13071; 1701pp + Sequence Listing; English.
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Pred. No. 2.3;
0; Mismatches 10; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 17939 GTGTGAGTGTGAATGTGTGGAATGTGTGAATGT 17979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX polynucleotide sequence SEQ ID NO:13151.
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75.6%;
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                                                                              11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
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2000US-0251990.
                         2000US-0251868
                                       2000US-0251869
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Best Local Similarity 75.6
Matches 31; Conservative
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Treated to as open reading frame, ORFX, whore X is 1-11491 (see Table In the specification).

In the specification, ABN15762 to ABN27552 encode the human ORFX proteins given in ABP0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated of its are useful for treating or preventing a pathology associated with an ORFX-associated disorder. ORFX polynocleotide syndrome associated with ORFX-associated disorder. ORFX polynocleotide sequences can be used in gene therapy. ORFX sequences can be used in the therapy. ORFX sequences can be used in the therapy. ORFX sequences can be used in the second disorders, carrivals of liver, psoriasis, benign tumours, keloid, degenerative disorders, insemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders infectious lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune disorders such as multiple sclerosis, infectious disease, autoimmune thyroiditis, myssthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfision injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Conservative
                                                                           29-MAY-2001; 2001WO-US10836
                                                                                                                                                           30-MAY-2000; 2000US-206132P
29-AUG-2000; 2000US-228716P
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nes 28; Conserv
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06-DEC-2001.
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2000US-0235836.
2000US-0236327.
2000US-0236367.
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  The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Expression and secretion vectors.
                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40402
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 21; Length 248;
Pred. No. 5.7;
1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 GTTTGAGAGAGAAGTGGGCCCAGGGGGCCAATGCGAGTAT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT 41
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 248 BP; 71 A; 48 C; 95 G; 34 T; 0 other;
                                                                                                               Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                    Claim 1; SEQ ID 26285; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK85590 standard; DNA; 75384 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180528.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
                                           21-FEB-2000; 2000EP-0200610.
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                                                                  99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 70.7
Matches 29; Conservative
                                                                                                                                   WPI; 2000-500381/45
                                                                                        (GEST ) GENSET
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                                                                  26-FEB-1999;
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
EP1033401-A2
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                     06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK85590;
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Gaps

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proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to produce the secreted (I), by inscrting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inscrting protein. (I) proteins and polynucleotides may be used to prevent and cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK4942 to AAK876950 and AAM8169 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; EST, probe; chemotractic; proliferative; immunomodulatory; haematopoietic; chemotractic; proliferative; immunomodulatory; haematopoietic; chemotractic; antipartial; antifundamatory; cytostatic; antibacterial; antifundamicory; antipartial; antidiabetic; autiasthmatic; vulnerary; antipartinonian; antiulcer; osteopathic; neuroprotective; nootropic; antipartisonian; antiulcer; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; haemophilia; thrombosis; laflammatory disorder; conduction disorder; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 75384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 75384 BP; 20654 A; 16699 C; 16073 G; 21958 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted expressed sequence tag SEQ ID NO:427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TGAGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA43852 standard; cDNA; 468 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-317938/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAA43852/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human immune/hematopoietic antigen polypeptides,
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2000US-0246475.
2000US-0246476.
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2000US-0246609.
2000US-0246610.
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2000US-0249215.
2000US-0249216.
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2000US-0249218.
2000US-0249244.
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2000US-0249264.
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                                                         20 - OCT - 2000;
01 - NOV - 2000;
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05-DEC-2000;
05-DEC-2000;
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08-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
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05-JAN-2001;
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P-PSDB; AAW27295.
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       AAA AAA43926 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTS), isolated from human, mouse, chicken and rat crissue sources. The SESTS can have a range of activities depending on the tissues they were isolated from. The activities include:

CC themotactic; proliferative; immunodulatory; haematopoietic; chemotinetic; analgesic; haemostatic; thrombolytic; antinfilammatory; cytostatic; antibacterial; antifungal; antivital; antidilabetic; antiasthmatic; vulnerary; antidicer; osteopathic; neuroprotective; cantiasthmatic; vulnerary; antidicer; osteopathic; neuroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the conformal swhich correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (authman), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (conficience (Alzheimer's, Parkinson's, Huntington's disease, stroke), coaqulation disorders (themothilia, thrombosis), inflammatory disorders (crohn's disease), tumours, bacterial, fungal or viral infections, depression and in the second of the second of the second of the second of sorders (parket) and sorders (crohn's disease), tumours, bacterial, fungal or viral infections, depression and succession and succession of the second of the second of sorders (crohn's disease), the second of the second of the second of the second of sorders (crohn's disease), the second of second of the second of s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 468 BP; 136 A; 106 C; 91 G; 135 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 TTTGAGAGAGAGTGTGCGCCTAAAACCACAGTGGGAGACT 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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96US-0635311
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Matches 28; Conserv
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Spaulding V;
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This cDNA sequence encodes the 5' end of a novel secreted protein, H83-22, which is isolated from a clone, H83-22 (ATCC 98028), derived from a human PBMC cDNA library. The nucleic acid and encoded H83-22 secreted protein can be used for research purposes (as markers for tissues, molecular weight markers for gels, primers, probes, etc.), for nutrition (as C, N or carbohydrate source), as a cytokine for cell proliferation and differentiation activity, as immune stimulants or suppressors e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or systemic lupus erythematosus, to requlate haematopoiesis, for tissue growth, as an activin or inhibin, or having chemotactic, chemokinetic, haemostatic and thrombolytic, receptor/ligand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; clone H83_22; peripheral blood mononucleocyte; PBMC; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Nucleic acids encoding novel secreted proteins - useful e.g. as an anti-inflammatory, immune stimulant or suppressor, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins - having many potential uses, e.g. as immunomodulators, cell proliferation or differentiation inhibitors or haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid clones from ATCC 98028 encode novel secreted
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                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 18; Length 479; Pred. No. 17;
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/transl_except= (pos:450..452, aa:Xaa)
/note= "Xaa= unknown; no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Racie LA;
                                                                                                                                                                                                                                                                                                                                            Sequence 479 BP; 139 A; 107 C; 92 G; 138 T; 3 other;
                                                                                                                                                                                                                                                                                                          anti-inflammatory or tumour inhibitory activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TGTGAGAGAGATGTGTGCYCTAAGTGTCAGTGTGAGTCT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lavallie ER, Mccoy JM, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
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138..479
                                                          81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  53.7%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5' fragment of clone H83_22.
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                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 28; Conserv
                                                        Claim 23; Page 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW36954.
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This sequence is the 5' portion of clone H83_22', which is a polynuclectide of the invention. This sequence was isolated from a human polynuclectide of the invention. This sequence was isolated from a human peripheral blood monouncleocyte (PBMC) cDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or considered protein, can be used, e.g. as a tissue or considered protein trap assays. The protein can be used to assay biological activity, raise antibodies for use in consect to assay biological activity, raise antibodies for use in the protein can be used to assay biological activities (no examples are given to support therapeutic and biological activities (no examples are given to support chis), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulator of cell proliferation and cifferentiation, immunostimulator, follicle inhibitor/stimulator, chemotactic/chemokinetic, haemostatic, thrombolytic or anti-inflammatory agent, antimicrobial, blorhythm, metabolism or behaviour modifier, anti-depressant or analgesic or psoriasis treatative.
                                                      Claim 44; Page 81; 114pp; English.
  regulators
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Sequence 479 BP; 139 A; 107 C; 92 G; 138 T; 3 other;

ó Gaps ; 0 53.7%; Score 22; DB 18; Length 479; 70.0%; Pred. No. 17; 1.1ve 1; Mismatches 11; Indels Query Match Best Local Similarity 70.0 Matches 28; Conservative

2 TGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT 41 a ò

Search completed: February 11, 2003, 02:05:52 Job time : 27.6596 secs

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AL077425 Drosophil
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BE892091 601344989
AR3728341 BB728341
BB728341 BB728341
AR372898 EST10599
AR314808 EST10599
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AR3131 BB694186
AR3131 BB694186
AR32350 AR32350
AL722438 AL722438
AL722350 AL722350
AL605933 Gallus ga
BE87045 EF637-1-0
BL275605 ULR-CWO-
AL21737 TELFROGON
AL31737 TELFROGON
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BG951973 CM4-CT062
AL002469 F.rubripe
AZ294343 RPCT-23-1
AL131211 Fugu rubr
BH118260 RPCT-24-2
AZ315242 1M0032F24
AZ315242 1M0032F24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1180 bp mRNA 11near EST 02-APR-2002 ACCOCCURT_6643098 NIH_MGC_121 Homo saplens cDNA clone IMAGE:5768406 BQ0007695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM12828 row: d column: 07

High quality sequence start: 3

High quality sequence stop: 536.

Logatlon/Qualifiers
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AQ762909 HS_3188_A
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AL722350
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AZ430586
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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LOCUS
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KEYWORDS
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B16867734 ft63a05.y
AL723525 AL723525
BRT56472 f15203.y
AQ069820 HS_2253_A
                                                                                         February 10, 2003, 20:51:09; Search time 118.283 Seconds (without alignments) 5613.764 Million cell updates/sec
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
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BASE COUNT

ORIGIN

Matches

AL723616/c DEFINITION

RESULT

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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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1 (bases 1 to 517)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                    BI867734 inhear EST 11-OCT-2001 ft63a05.yl Gong zebrafish ovary Danio rerio cDNA clone 5157800 5' similar to TR:Q06054 Q06054 ZINC FINGER PROTEIN 40.;, mRNA
                                                                                                                                                                                                                                                                       /dev stage="4-5 month"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary (pooled); Vector: pBluescript SK-:
Site_1: XhOI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
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AL/23525 Danio rerio embryonic inner ear subtracted cDNA Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Zhiyuan Gong for further information on this library (National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260). 118 q 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: zbrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
Seq primer: T3 ET from Annersham
High quality sequence stop: 399.
Location/Qualifiers
1. 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:7955"
/clone="15157800"
/clone=lib="Gong zebrafish ovary"
/sex="female"
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87.5%; Pred. No. 12;
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Matches 28; Conservative
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JOURNAL
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                                                                                                                                                                                                                                                        cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
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                                                                                                                                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7.3; Exb. Library is normalized and enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone_lib="Danio rerio embryonic inner ear subtracted
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 505)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., H.,J.P., Weissenbach,J. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio rerio)
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AL723516 Danio rerio embryonic inner ear subtracrerio cDNA clone BNOAA0672G01 5', mRNA sequence.
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/note="subtracted cDNA library"
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Pred. No. 12;
1; Mismatches
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                 /organism="Homo sapiens"
db_xref="taxon:9606"
/clone="IMAGE:5768406"
/clone=lib="MH_MGC_121"
/lab_host="DH10B"
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/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="BNOAA0672G01"
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Best Local Similarity 87.5
Matches 28; Conservative
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BASE COUNT ORIGIN

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send email to: info@image.llnl.gov
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AQ069820.1 GI:3389049
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illarity 87.5%;
Conservative
          Consortium/LLNL,
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Best Local Similarity
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

1 (bases 1 to 671)
S Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Marter, J., Maller, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Wylier, T., Underwood, K., Staptoe, M., Theising, B., Allen, M., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Washu Zebrafish EST Project 1998
Upublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing Dry: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E.
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1 (bases 1 to 595)
Columbra.R., Well.D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Welssenbach,J. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio rerio)
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY codex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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rerio cDNA clone BN0AA067zG01 3', mRNA sequence.
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Pred. No. 13;
1; Mismatches 3;
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/dev_stage="embryonic"
/note="subtracted cDNA library"
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/db_xref⊡"taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"BN0AA0672G01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 g
                                                                  AL723525.1 GI:20188129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 65.4%;
Best Local Similarity 87.5%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              embryonic inner ear
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                                                                                                                                     zebrafish.
Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
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ORIGIN
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JOURNAL
                                      ACCESSION
                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                      VERSION
KEYWORDS
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BF156472
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KEYWORDS
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                                                                                                                                     SOURCE
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/Gb_xref="taxon:7955"
/clone="3817540"
/clone="3817540"
/clone="3817540"
/clone="3817540"
/sugano Kawakami zebrafish DRA"
/sex="mixed (one male and one female, including
unfortilized eggs)"
/dev_stage="adult"
/lab_host="DH108 (phage resistant)"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); Ist strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT]
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTATGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site
CACCATGTG). Xhoi should be used to isolate the cDNA
insert Size selection was performed to exclude fragments
/l.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Kolchi Kawakami. Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACTGCAGCAGCAA."

17 a 140 c 141 g 173 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 358)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ069820 358 bp DNA linear GSS 05-AUG-1998 HS_2253_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col. Row-C, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jWallace@u.washington.edu
Sequence Tagged Connector
Plate: 2253 row: C column: 4
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26.8;
Pred. No. 14
                                                                                                                          /organism "Danio rerio"
Seg primer: T3 ET from Amersham
High quality sequence stop: 505.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTGTGAGAGAGATGTGTGCYCTAAGTGTCAG
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Location/Qualifiers
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source

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RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGCTCTTTTTTTTTTTTTTTV 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 13' end: Sall; 3' end: BamHI" 112 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS028NG 1003 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 245K23 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                 /tissue_type="mullerian duct includes surrounding region"
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodontidae, Tetraodon.

1 (bases 1 to 1003)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1003)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="6820447112"
/clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 GTGAGAGAGTATGTGTGCGGTGTGTGTGTGTGTGAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAG 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Score 25.2; 78.9%; Pred. No. 43
                                                /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                       female mullerian duct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                           /sex="female"
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A 112 C
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Matches 30; Conserv
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ORIGIN
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AUTHORS
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COMMENT
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SOURCE
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayafsu,M., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/sex="male"
                                                                                                                            /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                     Score 25.2; Pred. No. 38;
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75.0%;
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Best Local Similarity
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Query Match
Best Local Sim
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2
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Email: genome-res@gc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp,

A., Konno,H., Okazaki,Y., Hayatsu,N. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

agin.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

Hayashizaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/note="Genoscope sequence ID : C0AG245AF128F1~end
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Cycganisme_Tetraodon nigroviridis"
/db_xrefe"taxon:99883"
/clone="245K23"
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ilarity 75.6%; Pred. No. 80;
Conservative 0; Mismatches
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Contact: Yoshihide Hayashizaki
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SOURCE

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/clone_libe"REEN full-length enriched, CRL-2116 JC CDNA"
/cell_line="CRL-216 JC"
/note="pooled cell lines" (cell_line=RCR-1751 WEHI 164),
(cell_line=CRL-2116 JC), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0555 OHTA),
(cell_line=RCB-0559 K-1 . Fl), (cell_line=RCB-1283 B16
methoroma ), (cell_type=B cells, cell_line=RCR-1702 WEHI 231
), (cell_type=Leydig cells, cell_line-CRL-102 WEHI 231),
(cell_type=Leydig cells, cell_line-CRL-2055 MLTC-1),
(cell_type=Leydig cells, cell_line-CRL-2070 NE),
(tissue_type=bladder, cell_line-RCB-0544 MBT-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (tissue_type=bone marrow, cell_type=stroma cell,
cell_line=KCB-2028 SR-498), (tissue_type=colon,
cell_line=KCB-0649 Cle-H3), (tissue_type=colon,
cell_line=CCL-142 RAG), (tissue_type=submandibular gland,
cell_line=CRL-174 SCA-9 Clone I3), (strain=BABA/C,
cell_type=B cells, cell_line=CRL-1669 BCL1 Clone I3.20-383
), (strain=C3H, tissue_type=brain, cell_line:CRL-1443
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NH-MGC http://mgc.nci.nih.gov/.

NH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov a column: 21
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
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Pred. No. 58;
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/db_xrefo"taxon:10090"
/cloneo"IMAGE:5361692"
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High quality sequence stop: 531.
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/tissue_type~"retina"
                                                                                                                                                                                /db_xref="taxon:10090"
/clone="G430122H12"
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                                                                                        Location/Qualifiers
                                                                                                                                                /organism~"Mus
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Llarity 76.3%;
Conservative
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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               /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MCC Library."
                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR28C03 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                            Gaps
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae, Drosophila.
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/lab_host="DH10B (phage-resistant)"
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76.3%; Pred. No. 85;
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Pred. No. 99;
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/clone="BACR28C03"
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74.4%;
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RESULT 12

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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0158-270
600-008-d04&t3=2000-06-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence start: 20
Location/Qualifiers
BE706013 228 bp mRNA linear EST 12-SEP-2000 MR0-HT0158-270600-008-d04 HT0158 Homo sapiens cDNA, mRNA sequence.
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/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
/note_1: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                      1 (bases 1 to 228)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagail,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Fua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 49;
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/db_xref="taxon:9606"
/clone_lib="HT0158"
                                                                                      BE706013.1 GI:10094278
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AQ817531 434 bp DNA linear GSS 26-AUG-1999 HS_5249_A2_A04_SPGE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-825 Col∞8 Row~A, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 2 others
      /tissue_type."melanotic melanoma"
/lab_nost."bH10B (phage-resistent)"
/note="Organ: skin; Vector: pOMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Scrver:
http://www.htsc.washington.edu
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 1.4e+02;
1; Mismatches 9;
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Pred. No. 2.1e+02;
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/clonc="Plate:825 Coln8 RownA"
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University of Washington
401 Queen Anne Avenue North, Seattle, 1
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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Mahairas,G.G., Wallace,J.C.,
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/tlb.host="PHIOB (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library." 3 others
                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArC.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Library P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. II (bases 1 to 1667)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArcC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9750 row: b column: 23
High quality sequence stop: 129.
1 (bases 1 to 1329)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xrefu"taxon:9606"
/clone="IMAGE:4513601"
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-134-001C-2256
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US-09-754-250-3
US-08-77-217-4
US-08-76-534A-4
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3258
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Match 1
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                                                                                                   Perfect score:
                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                           Sequence:
                                                                                                                                                  Searched:
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                                                          Run on:
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APPLICANT: Sakamuro, Daitoku
TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: MYC-Interacting Protein (Bin1) and Uses Therefor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREETS Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
                                                   Sequence 3
Sequence 3
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US-08-222-177A-51
US-08-32-559-36
US-08-45-860-36
PCT-US95-0346-36
US-08-486-343A-3
PCT-US95-07349-3
US-09-407-562-32
US-09-407-562-31
US-09-407-562-31
US-09-407-562-31
US-09-407-562-31
US-08-970-269A-38
US-08-407-562-31
US-08-407-562-31
US-08-407-562-31
US-08-407-562-31
US-08-407-562-31
US-08-452-654-3
US-08-452-654-3
US-08-452-654-3
US-08-452-654-3
US-08-450-588-3
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FILING DATE:
CLASSIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,972
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOGLOFÉ, GATHY A,
REGISTRATION NUMBER: 33,980
RECISTRATION NUMBER: 33,980
RECISTRATION NUMBER: 33,980
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9200
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LOCATION: 680..765
OTHER INFORMATION: /note⊸ "exon 7"
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-870-126-11; Sequence 11, Application US/08870126; Patent No. 6048702; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 8310 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                   343
2997
2997
2997
11873
111878
111878
111883
3172
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.7%; Score 22; DB 3; Length 8310; Best Local Similarity 73.7%; Pred. No. 4.2; Matches 28; Conservative 0; Mismatches 10; Indels
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MADIUM TYPE: FLORY:

MEDIUM TYPE: FLORY disk

COMPUTER: IBM C compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NOWBER: US/09/445,247

FILING DATE: 03-Dec-1999

CLASSIFICATION: CURROWN>
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ADDRESSE: Howson and Howson
STREET: Spring House Corporate Cutr, P O Box 457
                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: exon
LOCATION: 5688..5929
OTHER INFORMATION: /note= "putative.alt.exon"
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FILING DATE: 06-JUN-1997
ATTORNEY FAGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60DPCT
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9818
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                        NAME/KEY: exon
LOCATION: 4059..4103
OTHER INFORMATION: /note= "exon 10"
FEATURE:
NAME/KEY: exon
LOCATION: 5543..5687
OTHER INFORMATION: /note= "exon 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: exon
; LOCATION: 7094..7221
USCHER INFORMATION: /note= "exon 12"
US-08-870-126-11
        NAME/KEY: exon
LOCATION: 1052..1127
OTHER INFORMATION: /note= "exon 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
                                                                                       NAME/KEY: exon
LOCATION: 2503..2585
OTHER INFORMATION: /note=
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COUNTRY: USA
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Sequence 6, Application US/08652972A

Patent No. 5723581

GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Sakamuro, Daitoku

TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: MrC-Interacting Protein (BIN1) and Uses Therefor NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 7093.,7221
CTHER INFORMATION: /note= "exon 12A"
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 5543..5687
OTHER INFORMATION: /note= "exon 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.7%; Sco. 73.7%; Pred. No. 4...
                                                                                                                                                                                                                                                                                                                                                                                                              /note= "exon 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/652,972A FILING DATE: 24-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 2503..2585
OTHER INFORMATION: /note=
                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FLILNG DATE: 05-WAY-1995
ATTORNEY/AGENT INFORMATION:
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LENGTH: 8310 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                             TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howson and Howson
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                         LOCATION: 680..765
OTHER INFORMATION:
                                                                                                                                                                                                                         LOCATION: 1052..11 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 4059..41 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match
Best Local Similarity 73.74
Matches 28; Conservative
                                                                                                                                                                                                NAME/KEY: exon TOCATION: 1052.
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Pennsylvania
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                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24
CLASSIFICATION:
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Sequence 6, Application PC/TUS9606231A
GENERAL INFORMATION:
APPLICANT: Wister Institute of Anatomy 8, Biology
TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: Myr-Interacting Protein (BINI) and Uses Therefor NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STRYE: Pennsylvania
CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19477
ZIP: TOOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: PCT/US96/06231A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /notem "unsequenced segment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASTETCATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WSTGOAPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9200
TELEPHONE: Q15-540-9200
TELEPHONE: Q15-540-9200
TELEPHONE: Q15-640-8018
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14985 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 1619..3174
COCATION: /noten "Exon 3"
POTHER INFORMATION: /noten "Exon 3"
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 325..1618
OTHER INFORMATION: /note
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LOCATION: 1332
OTHER INFORMATION: /
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 7209
OTHER INFORMATION:
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LOCATION: 1..324
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                  PCT-US96-06231A-6
                                                          RESULT 4
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                                                                                                                                                                                                                                                                                                                                    LOCATION: 1332
OTHER INFORMATION: /note= "unsequenced segment'
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "unsequenced segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "unsequenced segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAG 38
       31,215
3ER: WST60BUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 3175..4365
OTHER INFORMATION: /note= "Exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 4441..11518
OTHER INFORMATION: /note= "Exon 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 12241..14129
OTHER INFORMATION: /note~ "Exon 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
CCATION: 14130..14985
COTHER INFORMATION: /note= "Exon 9"
US-08-652-972A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 1..324
OTHER INFORMATION: /note= "Exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 1619..3174
OTHER INFORMATION: /note= "Exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 11519..11850
OTHER INFORMATION: /note" "Exon 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 11851..12240
OTHER INFORMATION: /note= "Exon 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 325..1618
OTHER INFORMATION: /note= "Exon 2"
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST6
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPHAX: 215-540-9200
SEQUENCE CHARACTERISTICS:
LENGTH: 14985 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (9enomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 3225
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 11097
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
LOCATION: 7209
                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
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LOCATION: 3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE: NAME/KEY: unsure
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LOCATION: 325.
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TOPOLOGY:
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Patent No. 56349492

GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
TITLE OF INVENTION: CHANNELS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: John W. Wallen III
STREET: 126 East Lincoln Avenue
CITY: Rahway
STARE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.7%; Score 22; DB 5; Length 14985; 73.7%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/435,933 FILING DATE: CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2336 GTGTGAGGGGGACTGTGTGACAGGTGTAAGTGTGTG 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: /note= "Exon 9" PCT-US96-06231A-6
LOCATION: 3175..4365
OTHER INFORMATION: /note= "Exon 4"
                                                                                                                                    NAME/KEY: exon
LOCATION: 11519..11850
OTHER INFORMATION: /note= "Exon 6"
                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 12241..14129
OTHER INFORMATION: /note= "Exon 8"
                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 11851..12240
OTHER INFORMATION: /note= "Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wallen, III John W.
REGISTRATION NUMBER: 35.4026
REFERENCE/COCKET NUMBER: 1926
TELECOMMUNICATION INFORMATION:
TELEFAX: (908) 544-3905
TELEFAX: (908) 54-4700
INFORMATION FOR SEQ ID NO: 5:
                                                     NAME/KEY: exon
LOCATION: 4441..11518
OTHER INFORMATION: /note-
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                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 14130..14985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 73.7
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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US-08-435-933-5
                                                                                                                                                                                                FEATURE:
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US-09-134-001C-2256/c

US-09-134-001C-2256, Application US/09134001C

Sequence 2256, Application US/09134001C

Patent No. 6380370

ENREAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                               Gaps
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                                                                                                             0;
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                                                                   51.2%; Score 21; DB 1; Length 3958; 69.2%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                     Sequence 5, Application PC/TUS9606035
GENERAL INFORMATION:
APPLICANT Arena, Joseph P.
APPLICANT: Paress, Philip S.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE TITLE OF ENVENTION: CHANNELS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%; Score 21; DB 5; Length 3958; 69.2%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jody M. Giesser
STREET: 126 East Lincoln Avenue - P.O. BOX 2000-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PACENTEN: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US96/06035 FILING DATE:
                                                                                                             11;
                                                                                                                                                                              114 GTGTGTGTGTGTTTTGTACATGTGCCAGTGTGAGT 152
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                                                                                                                                                        1 GTGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGT
                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Jody M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19264 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
INFORMATION 108, 594-4720
INFORMATION CR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 3958 base pairs
                                                          Query Match
Best Local Similarity 69.2'
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
; MOLECULE TYPE: CDNA
US-08-435-933-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rahway
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 27; Conserv
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PCT-US96-06035-5
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5570 GTCTGAGATAAATGTAAGCACTAAGTGTC 5599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, Junko
APPLICANT: Mulligan, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE TO STATEM TO STATEM TO SOFTWARE SOFTWAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20.4; DB 4;
Pred. No. 12;
                          CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 66/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
LENGTH: 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AAAATGTGTGCCATAAATATCAGTGTTATTTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208, Application US/08781891 Patent No. 6090620 GENERAL INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0%;
Matches 24; Conservative
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                                       GENERAL INCORNATION:
APPLICANT: WEI, MING-HUI et al
APPLICANT: WEI, MING-HUI et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING
TURRET REFERENCE: CL001063
CURRENT APPLICATION NUMBER: US/09/754,250
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRELES for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 111282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/472,217
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD 81928 GTCTCAGTGAGAAGTGGGGGCTCAGTGAGAGGTGAG 81965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.4; 1
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LCCATION: (1)...(111282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3
Sequence 3, Application US/09754250 Patent No. 6376225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/08472217; Patent No. 5726058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Alanen-Kurki, Leena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Auvinen, Petri
APPLICANT: Jaakkola, Panu
APPLICANT: Jalkanen, Markku
APPLICANT: Lepp, Sirpa
APPLICANT: Wall, Markku
APPLICANT: Vihinen, Tapani
APPLICANT: Wirinen, Tapani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20005
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                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                              LENGTH: 111282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-472-217-4
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Gaps

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DB 1; Length 2196;
                                                                                    Length 350;
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APPLICANT: Mali, Markku
APPLICANT: Mali, Markku
APPLICANT: Winnen, Tapani
APPLICANT: W rri, Anni
TITLE OF INVENTION: Syndecan Stimulation Of Cellular
TITLE OF INVENTION: Differentiation
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,217
                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1295 AAAGAGACTGCGTGCCTTCACTGCCTGTGTGAATC 1329
                                                                                                                                                                                                                                          146 AAAGAGACTGCGTGCCTTCACTGCCTGTGTGAATC 180
                                                                                                                                                                                                        6 AGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AGAGAGAATGTGTCTCTAAGTGTCAGTGTGAGTC 40
                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20.2; 1
Pred. No. 17;
                                                                                    Score 20.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1102.0050003
                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/472,217
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alanen-Kurki, Leena APPLICANT: Alanen-Kurki, Leena APPLICANT: Auvinen, Petri APPLICANT: Jaakkola, Panu APPLICANT: Jalkanen, Marku APPLICANT: Lepp , Sirpa
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08472217
Patent No. 5726058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                 49.38;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.38;
71.48;
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                                                                                                       Best Local Similarity 71.4
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-472-217-3
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                                                                                 Query Match
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APPLICANT: JALKANEN, MARKKU
APPLICANT: JALKANEN, PANU
APPLICANT: VIHLEN, TAPANI
TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN
TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,534A
FILING DATE: 0.2-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

49.3%; Score 20.2; DB 1;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 25; Conservative 1; Mismatches 9;
FILING DATE: 01-DEC-1>>c
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Mitchele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1102.0050003
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
FILEFAX: (202) 371-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CARACION NUMBER: 33,851
PPERRAPHOR JOCKET NUMBER: 1708.0050004/MAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F193/00514
FILING DATE: 01-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08760534A Patent No. 6017727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-760-534A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 350 base pairs
nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-08-760-534A-4
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ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
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APPLICANT: NARGO, Ken-ichi
APPLICANT: SEKO, Chisako
APPLICANT: KUROKAWA, Tsutcmu
APPLICANT: KONDO, Tatsuya
TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/340,820
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08340820 Patent No. 5512460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd2rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREE: 130 ....
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 65.9
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-222-177A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-340-820-24
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APPLICANT: Weber, James L.

TITLE OF INVENTION: (dc-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewlit Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                 APPLICANT: JALKANEN, MARKKU
APPLICANT: JAAKKOLA, PANU
APPLICANT: JAAKKOLA, PANU
APPLICANT: VIHINEN, TAPANI
TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN
TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                     STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,534A

FILING DATE: 02-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/206,186

FILING DATE: 07-MAR.1994

PRIOR APPLICATION NUMBER: PCT/F193/00514

APPLICATION NUMBER: PCT/F193/00514

FILING DATE: 01-DEC-1993

ATTORNEY/AGENT: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.3%; Score 20.2; DB 3; 71.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERNCE/DOCKET NUMBER: 1708.0050004/MAC
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 2196 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1295 AAAGAGACTGCGTGCCTTCACTGCCTGTGTGAATC 1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-222-177A-56/c
; Sequence 56, Application US/08222177A
; Patcnt No. 5582979
                                                                       Sequence 3, Application US/08760534A Patent No. 6017727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-760-534A-3
                                                      US-08-760-534A-3
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Gaps
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                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.8; DB 1;
Pred. No. 10;
1; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTGTGAGAGAATGTGTGTCTCAGTGTCAGTGTGAGTCT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/341,562
FILING DATE: 21-ARR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara. Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECHNON: (608) 831-2100
TELEFAX: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                    09865.601
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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## APPLICATION NUMBER: US/07/835,713
FILING DATE:
## ATTORNEY/AGGNT INFORMATION:
## NAME: CONLIN, David G.
## REGISTRATION NUMBER: 27026
## REGISTRATION NUMBER: 27026
## TELECOMMONICATION INFORMATION:
## TELEPHONE: (617)523-3400
## TELEFAX: (617)523-6440
## TELEFAX: (617)523-6440
## TELEFAX: (617)523-6440
## TELEFAX: (617)523-6440
## INFORMATION FOR SEQ ID NO: 24:
## SEQUENCE CHARACTERISTICS:
## INFORMATION FOR SEQ ID NO: 24:
## SEQUENCE CHARACTERISTICS:
## TOPOLOGY: Inhear
## MOLECULE TYPE: CDNA to mRNA
## POTHETICAL: NO
## ATPOTHETICAL: NO
## ORGANISM: HOMO SapienS
## APLOTYPE: 2 % IN
## CELL TYPE: Skin
## CELL TYPE: Than Inbrary
## CLONE: PGAFT
## US-08-340-820-24
```

Search completed: February 11, 2003, 06:00:08 Job time: 20.1156 secs

pp δy

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Gaps

Sequence 2820, Ap Sequence 7039, Ap Sequence 14184, A Sequence 531, App Sequence 217, App Sequence 277, App Sequence 1, Appl1 Sequence 1, Appl1 Sequence 1, Appl1 Sequence 1, Appl1

Sequence 11058, A Sequence 11058, A Sequence 11058, A Sequence 1580, Ap Sequence 1586, Ap Sequence 286, App Sequence 284, App Sequence 1, Appl Sequence 3, Appl Sequence 3, Appl Sequence 10, App Sequence 1023, App Sequence 1023, App Sequence 11, Appl Sequence 11, Appl

OM nucleic

Run on:

Sequence:

Searched:

Database

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US-09-962-436-276/c

Sequence 276, Application US/09962436

Settle Septence Septer, Daniel

TITLE OF INVENTION: Settle Septer Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 10; Length 1040;
Pred. No. 7.5;
1; Mismatches 11; Indels (
              0.5-09-874-2820

0.05-09-867-701-7039

0.05-09-864-701-1184

0.05-09-917-800A-1546

0.05-09-764-878-217

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0.05-09-946-807-1

10.05-09-864-761-11058

0.05-09-864-761-11058

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0.05-09-864-761-11058
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0 US-09-880-107-1586
0 US-10-108-605-286
US-10-108-605-286
US-10-108-605-286
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US-10-003-806-10
US-09-949-654-3
US-09-560-863-349
US-09-764-847-1022
US-09-878-574-5763
US-10-041-030-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 25, Application US/10114893; Publication No. US20020193567A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
PPPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
Query Match 53.7%;
Best Local Similarity 70.0%;
Matches 28; Conservative
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                                   465
499
608
6322
16854
98865
1503841
1503841
1503841
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11184
99916
173808
368004
246
3608
260
7136
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US-09-962-436-276
RESULT 2
US-10-114-893-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 276
LENGTH: 1040
TYPE: DNA
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Sequence 25, Appl
Sequence 20, Appl
Sequence 8075, Ap
Sequence 8075, Ap
Sequence 84, Appl
Sequence 84, Appl
Sequence 1149, Ap
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3691, Ap
Sequence 3691, Appli
Sequence 2, Appli
Sequence 52, Appli
Sequence 52, Appli
Sequence 52, Appli
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                                                                                                                                                       (without alignments) 5222.300 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  February 11, 2003, 03:31:30 ; Search time 3.72137 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NWB_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NWB_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NWB_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NWB_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 US-09-962-436-276

US-10-114-893-25

US-09-71-208-20

US-09-771-208-20

US-09-33-634-8

US-09-33-634-8

US-09-510-32-84

US-09-510-32-84

US-09-874-470-5

US-09-949-842-6

US-09-949-842-6

US-09-942-325A-2

US-09-942-325A-1

US-09-96A-761-7320

US-09-778-844-52

US-09-778-844-52

US-09-778-844-52

US-09-764-855-234
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         408267 seqs, 237001491 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                         US-09-942-310-2_COPY_860_900
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           nucleic search, using sy model
                                                                                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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1540
3449
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659158
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Query
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Gaps

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Result

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Pred. No. 7.5;
0; Mismatches 12; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N: MAP TO AL035665.22

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.2

N: EXPRESSED IN LUNG, SIGNAL = 0.89

N: EXPRESSED IN ADULT LIVER, SIGNAL = 6.7

N: EXPRESSED IN FETAL LIVER, SIGNAL = 10

N: EXPRESSED IN FETAL LIVER, SIGNAL = 15

N: EXPRESSED IN HELLO, SIGNAL = 1.9

N: EXPRESSED IN HELLO, SIGNAL = 1.9

N: EXPRESSED IN HELLO, SIGNAL = 4.6

N: EXPRESSED IN HERRY, SIGNAL = 4.6

N: EXPRESSED IN HERRY, SIGNAL = 4.6

N: EXPRESSED IN HERRY, SIGNAL = 3.3
   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTGTGAGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MEDRANO, JUAN
APPLICANT: MEDRANO, JUAN
APPLICANT: HORVAT, SIMON
FITULE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 4077-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US/08/999,477
FILING DATE: 1997-12-29
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ORGANISM: Mus musculus

ORGANISM: Mus musculus

PEATURE:
NAME/KEY: misc_feature

LOCATION: (123459)..(123478)

OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc_feature

LOCATION: (602466)..(602485)

OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc_feature

LOCATION: (546998)..(547017)

OTHER INFORMATION: n is unidentified a, c,
LOCATION: (494715)..(494814)

OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc_feature

LOCATION: (494715)..(494814)
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COCATION: (390986)..(391005)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc_feature
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Patent No. US20020155564A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ); OTHER INFORMATION: EXPRESSED
; OTHER INFORMATION: EXPRESSED
US-09-864-761-2538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.2%;
Best Local Similarity 70.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: E OTHER INFORMATION: E
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OTHER INFORMATION:
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SEQ ID NO 20
LENGTH: 659158
                                                                                                                                                                                                                                                                                                                                                         SEO ID NO 2538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-09-771-208-20
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·;
                           APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Bowman, Michael R.
APPLICANT: Spandiding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REPERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.7%; Score 22; DB 9; Length 1078; llarity 70.0%; Pred. No. 7.6; Conservative 1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PAPLICATION NUMBER: US 60/180,312
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-36
PRIOR PILING DATE: 2000-05-37
PRIOR PILING DATE: 2000-06-37
PRIOR PILING DATE: 2000-09-37
PRIOR PILING DATE: 2000-09-37
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2538, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
APPLICANT: Merberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-114-893-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 25
LENGTH: 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Gaps

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APPLICANT: Zuker, Charles S. APPLICANT: Zuker, Charles S. APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Wick
APPLICANT: Mucller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: NONEW CONTROL OF TAR, a No. US20030022278Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098010US
CURRENT APPLICATION NUMBER: US 09/510,332
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SOFTWARE: Patentin Ver: 2.1
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Alel Family of Taste Receptors
FILE REPERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Paten+T-
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Pred. No. 21;
1; Mismatches 11; Indels
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Patent No. US20020071842A1

GENERAL INFORMATION:

APPLICANT: Gumperz, Jenny E

APPLICANT: Brenner, Michael B

APPLICANT: Behar, Samuel M

TITLE OF INVENTION: Soluble CD1 Compositions and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 84, Application US/09510332; Publication No. US20030022278A1
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Best Local Similarity 69.2%;
Matches 27; Conservative
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Best Local Similarity 69.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8
LENGTH: 1540
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Futent No. US2002013237A1

GENERAL INFORMATION:

APPLICANT: Adjate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

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SOFTWARE FASTSEQ FOR WINDOWS VERSION 4.0
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Pred. No. 14;
1; Mismatches
                                                                                                                                   (346860)..(346823)
ORMATION: n is unidentified a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g, or t
US-09-771-208-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.2%;
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Adler, Jon Elliot
Ryba, Nick
Mueller, Ken
Hoon, Mark
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Best Local Similarity 69.2'
Matches 27; Conservative
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US-09-867-701-8075
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US-09-393-634-8
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TYPE: DNA LENGTH:

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Thu Feb 20 10:12:58 2003

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Gaps .; O

Indels

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Mismatches

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Conservative

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26;
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 Matches
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                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                  DB 10;
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                                                                                                                                                                                                                                                                                                                                             5679 AGAGAATTCTTGCTCTCAGTCTCAGTTTTTGTCT 5712
                                                                                                                                                                                                                                            Score 20.8; DE Pred. No. 40; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                         8 AGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.6; 1
Pred. No. 20;
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SEQUENCE DESCRIPTION: SEQ ID NO: 1149:
US-10-040-739-1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/040,739
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/036,520
FILING DATE: 03-JUN-1998
ATTORNEY/AGENT INFORMATION:
                 CURRENT TAPLICATION NUMBER: US/09/874,470
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,416
PRIOR FILING DATE: 2000-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1149, Application US/10040739
Patent No. US20020173635A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1149:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-Jan-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spaulding, vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Racie, Lisa
Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCoy, John
LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: U.S.A
                                                                                                            SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 10351
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70.3%;
                                                                                                                                                                                                                                              Query Match 50.7%;
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
 FILE REFERENCE: B00801/70212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
                                                                                            NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-874-470-5
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Best Local Similarity
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APPLICATION:
APPLICANT: Ni et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: Ni et al.
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/949,842
CURRENT APPLICATION NUMBER: US/09/949,842
CURRENT APPLICATION NUMBER: PCT/US01/07260
PRIOR FILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,367
PRIOR APPLICATION NUMBER: 60/2813
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3691, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PCOOS.
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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                      127 TATGAGAGTGTGCGTGTGCTGTGAGTGTGTGTGGG 163
2 TGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAG 38
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1; Mismatches
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Pred. No. 38
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                                                                                                                                    Sequence 6, Application US/09949842
Patent No. US20020164692A1
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70.3%;
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71.1%;
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Best Local Similarity 70.3%
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SOFTWARE: Patentin Ver 2.0
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Best Local Similarity 71.1
Matches 27; Conservative
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LENGTH: 2331
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US-09-942-325A-2
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SEQ ID NO 3
LENGTH: 111282
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US-09-864-761-7320
                                                    TYPE: DNA
                                                                                                      FEATURE:
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Petent No. US20020115179A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROSPHODIESTERASE PROTEINS, AND USES THEREOF
FILE REPERENCE: LOLO1063B1V
CURRENT APPLICATION NUMBER: US/10/094,989
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/754,250
PRIOR FILING DATE: 2001-01-05
                 APPLICANT: Kossler, Michael Applicants Kossler, Michael Applicants Kossler, Michael Applicants Kossler, Michael Applicants Foreign Hydroxlyase Promoter TITLE OF INVENTION: Sequence and Related Methods and Compositions File Reference: IACO1. NP001 CURRENT APPLICATION NUMBER: US/09/942,325A CURRENT APPLICATION NUMBER: 00/228931 PRIOR FILING DATE: 2001-08-29 PRIOR PAPLICATION NUMBER: 60/228931 PRIOR FILING DATE: 2000-02-30 NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 10828
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APPLICANT: ISCOVILLI, Lorraine
APPLICANT: Ressler, Mark
TITLE OF INVENTION: The Human Tyrosine Hydroxlyase Promoter
TITLE OF INVENTION: Sequence and Related Methods and Compositions
FILE REFERENCE: IACOI. MP001
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/228931
PRIOR FILING DATE: 2000-02-30
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Pred. No. 58;
1; Mismatches 12;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 13329
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Iacovitti, Lorraine
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 67.5%;
Matches 27; Conservative
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ORGANISM: Homo sapien
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US-10-094-989-3
                                                                                                                                                                                                                                                                                                              DNA
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RESIDENCE NO. SERVICANTIONS:
APPLICANT: REARL NO. SEZOROZOGUAR 57A1
GENERAL INPORMATION:
APPLICANT: REARL DAVIG K.
APPLICANT: REARLY. DAVIG K.
APPLICANT: REARLY. DAVIG K.
APPLICANT: REARLY. DAVIG K.
TITLE OF INVENTION: GENE EXPERSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPERSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: 12001-05-23
PRIOR PAPLICATION NUMBER: 12001-05-24
CURRENT FILLE DATE: 2001-05-24
PRIOR PAPLICATION NUMBER: 12001-05-26
PRIOR PAPLICATION NUMBER: 12001-05-26
PRIOR PAPLICATION NUMBER: 1200-05-26
PRIOR PAPLICATION NUMBER: 120
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LENGTH: 513
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Pred. No. 1e+02;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTGTGAGAGAGATGTGTGCYCTAAGTGTCAGTGTGAG 38
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Patent No. US20020048763A1
                                                                                                       ; LOCATION: (1)...(111282)
; OTHER INFORMATION: n = A,T,C or G
US-10-094-989-3
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.1%;
Matches 27; Conservative
                                                                      NAME/KEY: misc_feature
ORGANISM: Homo sapien
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; TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.6

OTHER INFORMATION: EXPRESSED IN HEALY, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8

OUR INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8

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Search completed: February 11, 2003, 09:10:30 Job time: 80.7214 secs

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PAT 18-MAY-2002

linear

DNA

Sequence 2 from Patent W00218638. AX394457 AX394457.1 GI:21065595

RESULT 1
AX394457
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

ALIGNMENTS

Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertobrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Risinger, C., Andersson, M.K., Lewander, T. and Ollasson, E. Detection of cyp2d6 polymorphisms Patent: WO 0218638-A 2 07-MAR-2002;

REFERENCE AUTHORS TITLE JOURNAL

M33386 Human CYLOC AX20724 Sequence AX58468 Human CYP2D M33189 Human Gebri M33387 Human debri AX345458 Sequence AX345459 Sequence AX345459 Sequence AX345459 Sequence AX365459 Sequence AX36545 Home sapi AC087389 Home sapi AC087389 Home sapi AC087389 Home sapi AC087389 Home sapi AC013274 Home sapi AC03124 Home sapi AC031274 Home sapi AC031327 Home sapi AC031324 Home sapi AC104532 Homo sapi AC004602 Homo sapi AC059778 Homo sapi AC028856 Homo sapi AC008521 Homo sapi AC008738 Homo sapi AC01317 Homo sapi AC011317 Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES AX207224 HSCYP2D7B HSCYP2D7A HUMCYP2DG HUMCYP8P AX34458 AX34458 AX34459 AX34559 AC007389 AC007389 AC007389 AC023574 AC01833 AX394457 AX394456 HUMCYP2D6 DB 72.6 114846 52.7 13278 52.7 13278 52.0 5884 32.0 5884 32.0 5884 10.7 191280 16.7 191280 16.7 191280 16.7 19281 16.1 1229950 16.0 182557 16.0 182557 16.0 182557 16.0 182557 17.0 0 182557 18.1 128950 Length 148876 175047 99.8 99.8 99.1 99.1 72.6 52.7 Match Query 1677.2 1665.4 1665.2 1220.4 885.4 872.8 537.4 2884.8 280.6 2280.6 273.6 273.6 271.2 268.8 268.8 268.8 268.2 264.4 264.2 264.2 264.2 264.2 264.2 263.6 263.6 Score Ş

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Detection of cyp2d6 polymorphisms
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Sequence 1 from Patent WO0218638.
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Pred. No. 0;
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22-NOV-1994 and Genet Euteleostom1; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Dases I to 9432)
Kimura, S., Umeno, M., Skoda, R.C., Moyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, ur 1140 1440 1440 1080 1140 1200 1260 1260 1320 1320 1380 1380 1500 1500 1560 1560 1620 1680 1680 Hum. CCTGGTGGGGGTGGGGTGCCAGGTGTGTCCAGAGGACCCATTTGGTAGTGAGGCAGGTA GGGGTGACTTCTCCGACCAGGCCCCTCCACGGCCTACCCTGGGTAAGGGCCTGGAGCAG CITIATAAGGGAAGGGTCACGCGCTCGGTGTGCTGAGAGTGTCCTGCGGTCCTCTGTG CTGAAGGTCACTCTGGAGTGGGCAGGTGGGGGTAGGGGAAAGGCCATGTTCTGGA GGAGGGGTTGTGACTACATTAGGGTGTATGAGCCTAGCTGGGAGGTGGATGGCCRGGTCC ACTGAAACCCTGGTTATCCCAGAAGGCTTTGCAGGCTTCAGGAGCTTGGAGTGGGGAGAG GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG GCAGCACACACACACAGCAGGTTCACTCACAGCAGAGGGCAAAGGCCATCATCAGCTCC CCTGGTGGGGTGGGGTGCCCAGGTGTCTCCAGAGGAGCCCCATTTGGTAGTGAGGCAGGTA TGGGCCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCGTGG ٦. . NA linear PR. gene, complete cds for [Am. Draft entry and computer-readable sequence 45, 889-904 (1989)] kindly submitted by S.Kimura, 29-MAR-1990.
Location/Qualifiers Genet. 45 (6), 889-904 (1989) DNA P450 IID6 Human cytochrome P450 IID6 (CYP2D6) cytochrome P450; cytochrome P45 Human DNA, clone lambda2D-18/2.

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	1201 GGAGGGTTGTGACTACATTAGGGTGTATGAGCCTAGCTGGCAGGTGGATGGCCRGGTC 126	
Qy 121 GGTG Db 121 GGTG	OY 1141 CTGAAGGTCACTCTGGAGTGGGCAGGTGGGGAAAGGCCAAGGCCATGTTCTGGA 1200 	
Oy 61 AGC: Db 61 AGC:	OY 1081 ATGCCACTCATCATCAGGAGCTCTAAGGCCCCAGGTAAGTGCCAGTGACAGATAAGGGTG 1140 	
Qy 1 GAA: Db 1 GAA:	GTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATG 108	
ORIGIN Query Match Best Local 6 Matches 1666	901 GTGFATGTGTGTGTGTGTTTGTGTGGGTGATTTTCTGCGTGTGTGT	
FEATURES SOURCE SOURCE BASE COUNT ORIGIN	QY 841 ATGTGTGTGTGTGTGTGAGAGAGAATGTGTGCXCTAAGTGTCAGTGTCAGTGTCAGTGTCAGTGTCAGTGTCAGTGTCAGTGTCAGTGTGAGTGT 900 Db 841 ATGTGTGTGACTGTGTGAGAGAATGTGTCCCTAAGTGTCAGTGTTAGTGTGTGAATAGTGTTATGTGTGAATAGTGTTATGTGTGAATAGTGTTATGTGTGGGTGATTTTCTGCGTGTGAATCGTGTCCCTG 960 Db 901 GTGTAATGTGTGAATATTGTGTGGGGGTGATTTTCTGCGTGTGATATCGTGCCCTG 960	
ORGANISM STATEMENT ORGANISM STATEMENT OF TITLE PROUDLY OUT OF TITLE OR TOWN OF THE ORGANISM OF THE ORGANISM ORG	Oy 721 CATAGCCCGGCCAGGAATGTGGGCTGGGCTGGGACAGCCTTGGACAGGAGT 780 111111111111111111111111111111111111	
ACCESSION AND VERSION AND KEYWORDS	Oy 661 CAAGGCCTTCCGGCTACCAACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGG 720 	

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AX207224 1 from Patent W00155432.

RESULT 4 AX207224 LOCUS DEFINITION

Polymorphisms in the human cyp2d6 gene promoter region and their use in diagnostic and therapeutic applications
Patent: WO 0155432-A 1 02-AUG-2001;
Epidauros Biotechnologie AG (DE) 240 240 120 180 180 300 300 360 360 420 420 480 540 540 900 99 099 720 PRGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120 600 CAAGGCCCTTCCGGCTACCAACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGC 720 Gaps 9 9 TGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC ATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACAAAATT **ATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAAATCTCCGTCTC** SAACAAAGGATCCTCCATAACGTTCCCACCAGATTTCTAATCAGAAACATGGAGGCCA AAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAGGATGTTGTCACAGGCTGGGG **AAAAAAAAAAAAAAAAAAAAAGRATTAGGCTGGGTGGTGCCTGTAGTCCCAGCTACTT** SAGGCAGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGCCACTGCAC ó Length 1669 others 0; Indels 8 . 9 /organism-"synthetic construct" /db_xref="taxon:32630" /note-"artificial sequence" DB ىد 99.1%; Score 1665.4; 99.8%; Pred. No. 0; live 3; Mismatches 338 Location/Qualiflers 1. .1669 534 g synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 1669)
Raimundo, S. and Zanger, U. GI:15394976 376 c 66; Conservative Similarity 4X207224.1 ø 413 D Z ò

us-09-942-310-2.rge

<pre>Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 13677)</pre>	Heim, M.H. Direct Submission Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre	ingelk		See X584	/db_xref="taxon:9606" /chromosome="22" /clone="45" /clone lib=PMR14"	/dev_stage="adult" 1534. 5868 /gene="CYP2D78P" join(1534. 1801.2504. 2675.3203. 3358.2444. 2606.	40314207,44004540,47354922,53775518,56175868) //gene="CYP2D7BP" 15341801 //qene="CYP2D7BP"	/number=1 join(1622. 1801,25042675,32033355,34443605, 40314207.44004540,47354922,53775518,56175795) /gene="CYP2777P"				3203. 3355 /gene="CYP2D7BP" /number=3 3356 3443	/gene="CYP2D7BP" /number=3 3444, 3505 /gene="CYP2D7BP"	/number=4 36064030 /gene=-CYP2DD7BP" /number=4	40314207 /gene=""CYP2D7BP" /number=5 42084399	/gene="CYP2D7BP" /number=5 44004540 /gene="CYP2D7BP"	/number=6 4541. 4734 /dene="YYPJD7AP"	/dumber=6 47354922 /gene="CYP2D7BP" /number=7
REFERENCE	AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED	COMMENT FEATURES SOUFCE		gene	exon	CDS	intron	exon	intron	exon	exon	intron	exon	exon	intron	exon
	VY /81 GGTCCCATCAGGAAACTTCCGGCATGGCTGGGAAGTGGGGTACTTGGTGCCGGGTCTGT 840	Oy 841 ATGTGTGTGTGGGTGTGTGTGGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT 900	OY 901 GIGTANGIGIGAATATIGICTITIGIGIGGGGGATITITICIGCRIGIAATCGIGICCCTG 960	OY 961 CAAGTGTGAACAAGTGGACAGGGGTGGACAGAGAGATCTGTGCACCATCAGGT 1020 	OY 1021 GTGTGCATAGCGTCTGTGCATGTCAAGAGTGAAGTGAAG	OY 1081 ATGCCACTCATCAGGAGCTCTAAGGCCCCAGGTAAGTGCCAGTGACAGATAAGGGTG 1140	QY 1141 CTGAAGGTCACTCTGGAGTGGGCAGGTGGGGGAAAGGCCAAGGCCATGTTCTGGA 1200 DD 1141 CTGAAGGTCACTCTGCAGTGGGCAGGTGGGGGTAAGGCAAAGGCCATGTTCTGGA 1200	QY 1201 GGAGGGGTTGTGACATTAGGGTGTATGAGCCTAGCTGGGGGGGG	OY 1261 ACTGAAACCCTGGTTATCCCAGAAGCTTTGCAGGCTTCAGGAGCTTGGAGTGGGGAGAG 1320	QY 1321 GGGGTGACTTCTCCGACCAGGCCCTCCACCGGCTACCCTGGGTAAGGGCCTGGAGCAG 1380 	OY 1381 GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCGGCCTGGCCTGACTCTGCCACTG 1440	OY 1441 GCAGCACAGTCAACAGAGGTTCACTCACAGCAGAGGGCAAAGGCCATCATCAGCTCC 1500	QY 1501 CTTTATAAGGAAGGTCACGCGCTCGGTGTGCTGAGAGTGTCCTGCTGGTCCTCTGTG 1560	Oy 1561 CCTGGTGGGGTGCCAGGTGTGTCCAGAGGCCCATTTGGTAGTGAGGCAGGTA 1620 Db 1561 CCTGGTGGGGTGCCAGGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTA 1620	OY 1621 TGGGGCTAGAAGCACTGGTGCCCTGGCGTGATAGTGGCCATCTTCCT 1669	acucanon	DEFINITION Human CYP2D7BP pseudogene for cytochrome P450 2D6. ACCESSION X58468	VEKSION ASB408.1 61:3033/ KEYWORDS CYP2D7Bp gene; Cytochrome P450; cytochrome P450 2D6; pseudogene. SOURCE Homo sapiens. ORGANISM Homo sapiens

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/note-"ACCCTTCCCC"
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4923. .5376
/gene~"CYP2D7BP"
                                                5519. .5616
/gene="CYP2D7BP"
                                                                         5617. .5868
/gene-"CYP2D7BP"
                        5377. .5518
/gene::"CYP2D7BP"
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Best Local Similarity 99.5%;
Matches 1673; Conservative
                                                                /number-8
5617. 586
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/ Once="Lip repeat: matches 2294. .2311 of consensus" 21270. .22130 / Anote="Lip repeat: matches 1445. .2294 of consensus" / Anote="Lip repeat: matches 1370. .1445 of consensus" 22425. .22994 / Anote="Lip repeat: matches 1370. .1445 of consensus" 22502. .22994 / Anote="Lip repeat: matches 1. .510 of consensus" / Anote="BaEV-int repeat: matches 4243. .6625 of consensus" 25379 / Anote="match: STS: Em:G07321" / An
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7061e="LiPBa repeat: matches -656. .1226 of consensus" 37163. .37323  
7061e="Earlequin repeat: matches -912. .1086 of consensus" 73724. .37437  
73724. .37437  
706e="57 copies 2 mer ga 79% conserved" 706e="57 copies 2 mer ga 79% conserved" 7001e="match: STS: Em:G27508"  
7001e="match: STS: Em:G47808"  
7001e="match: STS: Em:G43129"  
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7.10ve- match: CDS: EM:AZ08330"
7.10ve- "HERVI repeat: matches 4455. 5408 of consensus"
7.8386. 30853
7.00te- "HERVI repeat: matches 2098. 4455 of consensus"
7.00te- "HERVI repeat: matches 2098. 2163 of consensus"
7.00te- "HERVI repeat: matches 2098. 2163 of consensus"
7.00te- "HERVI repeat: matches 1561. 2163 of consensus"
7.00te- "HERVI repeat: matches 1561. 2163 of consensus"
7.00te- "HERVI repeat: matches 9. 1561 of consensus"
7.00te- "HERVI repeat: matches 1561. 2163 of consensus"
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7.00te- "IIRNI repeat: matches 1. 510 of consensus"
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              17434. .17688
/note="LIMD repeat: matches 1222. .1482 of consensus"
19152. .19153
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19896. 19939
700te="LIP repeat: matches 2416. 20246. 20284
70ote="LIP repeat: matches 2378. 32594. 20660
70ote="LIP repeat: matches 2311. 320965. 20965. 20982
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complement(26269. 26446)
/note="match: GSS: Em:AF046780"
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/note="CpG island"
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                                                                                                                                                                                                                                                                                                                                      Auguritaced (124-7007-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK E-mail enquiries: Institute, Hinxton, humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Nov 25, 2001 this sequence version replaced gi:3204432.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at their source databases:

on the WORMPEP database can be found at the content of the covered by high quality data (i.e., pired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by thigh quality data (i.e., pired quality >= 30); and attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by the sassembly was confirmed by the sanger confirmed by the sanger confirmed by the sanger contings of human chromosome 22 mapping Group.

Futher information can be found at the sequence of the confirence of the
                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 114846)
Bridgeman, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/HGP/Chr22
RPI-257120 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                               Direct Submission
Submitted (22-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VECTOR: pcrPAC2
This sequence is the entire insert of clone RPI-257120 The true right end of clone RPI-18601 is at 20171 in this sequence.
Location/Qualifiers
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/note="LIMD repeat: matches 1552. .1964 of consensus" /note="LIMD repeat: matches 1482. .1552 of consensus" /note="LIMD repeat: matches 1482. .1552 of consensus"
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7162. 7366
/note="match: STS: Em:HS324WC5"
7357. .7396
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1097. 1600
Anote="match: GSS: Em:AQ563517"
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/note="match: GSS: Em:AQ140240"
4148. .4647
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/note="match: GSS: Em:AQ124532"
13208. 14275
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/chromosome="22"
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/clone_lib="RPCI-1"
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/note="CpG island"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485
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Em:G27630"
                                                                                                                                                           mer cc 75% conserved".69374)
Em:B14383"
                                                                18 copies 2 mer aa 80% conserved"
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                                                                                                                                                                                                                                                                                                                                                                              note-"MER21B repeat: matches 76.
15375. .85430
                                                                                                                                                                                                             complement(78378, 78961)
/note:"match: GSS: Em:AQ389013"
complement(78421, 78533)
/note:"match: GSS: Em:AQ42556"
complement(78451, 78977)
/note:"match: GSS: Em:AQ533248"
complement(81846, 82274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                           cumptement(81846, .83274)
/note="match: GSS: Em:A0618257"
82587, .83003
/note="LIMMSA repeat: matches 58
                                                                                             Em: AQ617313"
                                                                                                                                        Em: AQ044403"
                                                                                                                                                                                                        Em: AQ181535"
                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-"11 copies 2 mer ac 100%
                                                                                                                   Em: AQ084812"
          Em: AQ035975
                                                                                                                                                                                                                                                                                                                                                                                                 /note="28 copies 2 mer aa 76% complement(90629. .90900) /note="match: GSS: Em:B13983"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1220.4;
Pred. No. 0;
5; Mismatches
                                                                                                                /note="match: GSS: En
66603. .66893
/note="match: GSS: En
66974. .67017
/note="22 copies 2 m
complement(69196. .6
                                                                                                                                                                               /note="match: GSS:
69710. .70103
/note="match: GSS: 1
                                                 /note="match: STS:
66514. .66549
                               /note="23 copies 2
                                                                                            /note="match: GSS:
66577. .66930
                                         complement (65929
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Similarity 90.6%;
36; Conservative
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                  GCAAGGTGAAGTGAAGGGACCAGGCCCATGATGTCATCATCATCAGGAGCTCTAAGGCC
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996 ACAAGAGATCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAG 1055
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ilarity 97.1%; Pred. No. 1.1e-244;
Conservative 3; Mismatches 24;
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/note="ACCCTTCCCC repeat"
3664 c 3968 g 2744
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3651. .3827
/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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3651. .3827,4020. .4161,4356. .4542,4998. .5139,5238. .5489)
7/gene="CYP2D7AP"
1154. .1424
/gene="CYP2D7AP"
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3651. .3827,4020. .4161,4356. .4542,4998. .5139,5238. .5416)
/gene="CYP2D7Ap"
                                                                                                                                                                                                  PRI 21-0CT-1992
                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre
University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND
2 (Basel, Mal278)
Heim, H. and Meyer, U.A.
Evolution of a highly polymorphic human cytochrome P450 gene
cluster: CYP2D6
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13278)
50382 AGAGGAGCCCAGTAGGTAGTGAGGCAGCCATGGGGCTAGAAGCACTGGTGCCCCTGGCCA 50323
                                        1591 AGAGGAGCCCATTTGGTAGTGAGGCAGGTATGGGGCTAGAAGCACTGGTGCCCCTGGCCG 1650
                                                                                                                                                                                                                                   XS8467.1 GI:30336
CYP2D7AP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See X58468, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
                                                                                                                                                                                       HSCYP2D7A 13278 bp DNA linear
Human CYP2D7AP pseudogene for cytochrome P450 2D6.
X58467
                                                                                                                1651 TGATAGTGGCCATCTTCCTGCTCCTGGTGG 1680
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/db_xref="taxon:9606"
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/db_xref="PID:e34292"
1425. .2124
/gene="CYP2D7AP"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 14 (1), 49-58 (1992) 93052308
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1154. .5489
/gene="CYP2D7AP"
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/gene="CYP2D7AP"
/number=3
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2125. .2296
/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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/gene="CYP2D7AP"
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Homo sapiens
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HSCYP2D7A
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KEYWORDS
SOURCE
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ESGFLREVLNAVPVLLHIPALAGKVLRFQKAFLTQLDELLTEHRMTWDPAQPPRULTE
FALABKERKKONPESSENDBULRIVADLESAGWYTSTFTAMGLLLAUTHPDVORRV
QQEIDDVIGOVRRPENGDQAIMPYTTAVIHEVQRFGDIVPLGVTHMTSRDIEVGFFI
PKGTTLITNLSSVLKDEAVWEKPFRFHPEHFLDAQGHFVKPEAFLPFSAGRRACLGEP
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/note-"debrisoquine 4-hydroxylase intron
2661. .2820
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/note∵"debrisoquine 4-hydroxylase intron
                                                                                                                                                                           994. .1695
/note⇔"debrisoquine 4-hydroxylase intron
                                                                                                                                                                                                                                                                1878. .2418
/note⊳"debrisoquine 4-hydroxylase intron
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                                                                                                             <814. .993
/note:"debrisoquine 4-hydroxylase'
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Pred. No. 4.7e-241;
3; Mismatches 0;
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/note: "debrisoguine
3970. .4157
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/note:"debrisoquine
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/note="debrisoquine
4612. .4753
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/note="debrisoquine
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/note-"debrisoguine
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llarity 99.7%;
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/number=6
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2572. .266
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Chromosome 22.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="total"
/db_yref="total"
/db_y
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5503)
Gonzalez,F.J.
Unpublished (1990)
Draft entry and computer-readable sequence for [1] kindly submitted by F.Gonzalez, 23-MAR-1990, for release after publication.
Author address: F.Gonzalez
National Cancer Institute
Bldg. 37 Rm. 38-24
National Institute of Health
Bothesda, Md 20892.
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PVPITQILGFGPRSQGKQRGVPGALWARVARAEALLRLHLAQLGPGQEVAGAVGDRGG
RLPLCRLRQPLRRPFRPNGLLDKAVSNVIASLITCGRRFEYDDPRFLRLLDLAQEGLKE
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Human debrisoquine 4-hydroxylase mutant allele (CYP2D6-MA1) gene,
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                                      TACCCTGGGTAAGGGCCTGGAGCAGGAAGCAGGGGCAAGAACCTCTGGAGCAGCCCATAC
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                                                                                                         CTTCAGGAGCTTGGAGTGGGGAGAGGGGGGTGACTTCTCCGACCAGGCCCCTCCACCGGCC
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Human individual MAGA DNA.
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oin(11324. 11504,12206. 12377,12906. 13058,13147. 13307, 3733. 13909,14102. 14243,14438. 14625,15080. 15221, 5320. 15496)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer-readable sequence for [1] kindly submitted by S.Kimura, 29-MAR-1990.

Location/Qualifiers
1. .17660
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Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4-hydroxylase (CYP2D) Locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                             CTTTGCAGGCTTCAGGAGCTTGGAGTGGGGAGAGGGGGTGACTTCTCCGACCAGGCCCCT 1346
                                                                                                                                             CCACCGGCCTACCCTGGGTAAGGGCCTGGAGCAGGAAGCAGGGGCAAGAACCTCTGGAGC 1406
                                                                                                                                                                                                                                                  CTCACAGCAGAGGCCAAAGGCCATCATCAGCTCCCTTTATAAGGGAAGGGTCACGCGCTC 1526
                                                                                                                                                                                                                                                                                                    GTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTATGGGGCTAGAAGCACTGGTGCCCCTG 1646
                                                      540
TATGAGCCTAGCTGGAGGTGGATGGCCRGGTCCACTGAAACCCTGGTTATCCCAGAAGG
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debrisoquine 4-hydroxylase.
Human DNA, clones lambda-2D-A and lambda-2D-B.
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/codon_start=1
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AGGAGCCCATTTGGTAGTGAGGCAGGTATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTG
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                                                                                                Sequence 529 from Patent WO0200928.
AX345458
AX345458.1 GI:18493344
                                              1653 ATAGTGGCCATCTTCCTGCTCCTGGTGG 1680
                                                                                                                                                                                                                  Location/Qualifiers
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Matches 1086; Conservative
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/db_xref:"taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Pred. No. 2.1e-207;
5; Mismatches 386;
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                                                                      Score 537.4; DB 6;
Pred. No. 4.5e-144;
5; Mismatches 506;
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                                                                      Query Match 32.0%;
Best Local Similarity 62.4%;
Matches 949; Conservative
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GGGAAAGGGCAAGGCCATGTTCTGGAGGAGGGGTTGTGACTAACATTAGGGTGTATGAGCC 1234
                                               AAAAAAAAACAAAATCATATTCTAAAAAAAATTTATAACTACATTAAAATATATAAAAC 1270
                                                                  TAGCTGGGAGGTGGATGGCCRGGTCCACTGAAACCCTGGTTATCCCAGAAGGCTTTGCAG 1294
                                                                               CTACCCTGGGTAAGGGCCTGGAGCAGGAAGCAGGGCAAGAACCTCTGGAGCAGCCGATA 1414
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/note="chemically treated genomic DNA (Homo sapiens)"
92 c 1381 g 2681 t
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3576. .3688
/note="GRAIL 2 excellent exon, frame 0"
complement(4146. .4250)
/rpt_famlly="Alu"
4282. .43n?
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complement(11675. .12012)
/rpt_family="THEI"
complement(12115. .12401)
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complement(9121. .9458)
/rpt_family~"L1"
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16347. 16367
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2806. 1202.
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/noter"(T)22"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 78065)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Sequencing of human chromosome 5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC005355 78065 bp DNA linear PRI 31-JUL-:
Homo sapiens chromosome 5, Pl clone 1307e8 (LBNL H60), complete
                                        1355 CTACCCTGGGTAAGGGCCTGGAGCAGGAAGCAGGGGCAAGAACCTCTGGAGCAGCCCATA 1414
                                                                                                        1475 AGAGGGCAAAGGCCATCATCAGCTCCCTTTATAAGGGAAGGGTCACGCGCTCGGTGTGCT 1534
                                                                                                                                                                                                                                                                                      1535 GAGAGTGTCCTGCCTGGTCCTCTGTGCCTGGGGGTGGGGGTGCCAGGTGTCTCAGAG 1594
                                                                                                                                                                                                                                                                                                                                                                              1595 GAGCCCATTTGGTAGTGAGGCAGGTATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGAT 1654
                                                                                                                                                                                                                         Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
Unpublished
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AC005355 AC001062 L81708 L81709 L81710 L81882 L81883
AC005355.1 GI:3366557
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69. .96
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/rpt_unit~AGGG
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Ricke, D.O.
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us-09-942-310-2.rge

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.. 2370. .25510

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complement(26535. .26624)

/note="GRAIL 2 excellent exon, frame 1"

complement(26705. .26996)

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36311. 36882
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37120. 37382
                                                                      complement(20237, 20537)
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complement(23803.
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4 EUKaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 191280)

Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP11-304114

Unpublished 2 (bases 1 to 191280)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., AC087389 191280 bp DNA linear HTG 21-AUG-2002 HOMO sapiens chromosome 17 clone RP11-304114 map 17, WORKING DRAFT SEQUENCE, 7 unordered pieces. 53712 53652 53592 299 TIGCATCATIGCACAAIGGAGGGAGCCACCAGCCIGGGCAACAAGAGGAAAICICCGIC 358 Gaps 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAAAAATT 60 61 AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 121 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC 239 AGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGA 181 TCTACTGAAAATAYAAAA--AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTT TTGGGAGGC-----AGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGC 24; Length 78065; Score 284.8; DB 9; Length 7 Pred. No. 5.9e-71; 3; Mismatches 105; Indels AC087389.2 GI:22381544 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP /rpt_family="MER7"
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40790. .41056
/rpt_family="Alu"
42301. .42473
42481. .42768 17.0%; 75.6%; Query Match Best Local Similarity 75.6' Matches 410; Conservative Homo sapiens repeat_region repeat_region repeat_region repeat_region repeat_region 53305 AA 53304 human. 533 AA 534 LOCUS DEFINITION 419 ORGANISM RESULT 15 AC087389 REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE Dp ŏ δχ ò δ Pp Dp pp à δy qq ŏλ Qγ q QΣ

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                             43104 43203: gap of 100 bp
43204 48527: contig of 5324 bp in length
48528 48627: gap of 100 bp
55133 55232: gap of 100 bp
55233 106632: contig of 5100 bp in length
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                                                                                                                      42841: contig of 42841 bp in length
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42942 43103; contig of 162 bp in length
43104 43203; gap of 100 bp
43204 48627; contig of 5324 bp in length
48528 48627; gap of 100 bp
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53969 a 41905 c 41245 g 53558 t
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Barna, N., Bastlen, V., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chararo, B., Choepel, Y., Collymore, A., Canang, J., Chararo, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, M., Hagos, B., Horton, L., Hulme, M., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Luu, G., MacCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Mienga, V., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Sanje, T., Topham, K., Travers, M., Vassiliev, H., J., Shaner, A. and Zody, M., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilse, B., Street, Cambridge, M. Ollu, J., Sanger, Camber, S., Schupbam, K., Travers, M., Vassiliev, H., J., Lamer, A. and Zody, M., Waran, D., Young, G., Zalnoun, J., Labmitted (21-AuG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, M. Ollu, J., Sanger, Cambridge, M. Ollu, J., Shane, S., Shall, A.F., & Green, P. (1996-1997)

All repeats were identified using RepeatMasker: html

Leneats were identified using RepeatMasker: html

Leneats were identified using RepeatMasker: html

Conter: Whithchead Institute/MIT Center for Genome Center: Whithchead Institute/MIT Center for Genome Center: Whithchead Institute/MIT Center for Genome Center: Whithchead Institute/MIT Center for Genome Center.
  Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 191280)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * arbitrary. Gaps between the contigs are represented as
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Insert size: 190880; sum-of-contigs
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
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Web site: http://www-seq.wi.mit.edu
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COMMENT

Db 108898 GAGTTCAAGACCAGCCTGGCCAACATGGCGAAACCCCATCTCTACTAAAAATACAAAAGT 108957 Db 109012 GGTGGATCACCTGAGGTCGGAGATTGAGACACCTGACCAACATGGAGAAATCCCATC 109071 Db 108958 GGCC-----GGGTGCGGTGCCTCATGCCTGTAATCCCAGCACTTTGGAAGGCCGAAGCG 109011 Db 109132 AGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGAAGGCAGAGGTTGCGGTGAGCCGAGA 109191 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATT 61 AGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 299 TTGCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTC 121 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC 181 TCTACTGAAAATAYAAAA--AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTT 239 AGGAGGCTGAGGCAGGAGATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGA DB 2; Length 191280; 87; Indels 603 others Pred. No. 1e-69; 3; Mismatches 16.7%; Score 280.6; 76.4%; Pred. No. 1e-

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Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenoblotic; ligase-based sequenced determination; drug metabolism; chromosome 22; gene; polymorphism; ds.
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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 26 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human CYP2D6 gene 5' flanking region containing polymorphic sites.
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ó 120 180 180 240 240 300 300 360 Gaps 9 9 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATT 61 AGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC TCTACTGAAAATAYAAAAAGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAG GCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTCTC GAGGCTGAGGCAGGAGATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATT DB 24; Length 1680; ó; Indels Sequence 1680 BP; 413 A; 379 C; 539 G; 342 T; 7 other; 0; 99.8%; Score 1677.2; 100.0%; Pred. No. 0; Pred. No. 0; 0; Mismatches 100.08; Query Match 99.8 Best Local Similarity 100. Matches 1680; Conservative 61 121 121 181 181 241 241 301 301 361 ò a ò g δλ g δ g g ò Ωÿ 엄

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1020 1080 1140 1200 GGGGTGACTICTCCGACCAGGCCCCTCCACCGGCCTACCCTGGGTAAGGGCCTGGAGCAG 1380 480 480 009 600 099 099 720 780 840 720 780 900 900 960 GGGAGGCAGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGCCACTGCAC GAAAGCAGTGGAGGAGACRACCCTCAGGCAGCCCGGGAGGATGTTGTCACAGGCTGGGG 721 CATAGCCCGGCCAGAGCCCAGGAATGTGGGGTTGGGCTGGGAGCAGCTTTGGACAGGAGT ACTGAAACCCTGGTTATCCCAQAAGGCTTTGCAGGCTTCAGGAGCTTGGAGTGGGGAGAG CTGAACAAAGGATCCTCCATAACGTTCCCACCAGATTTCTAATCAGAAACATGGAGGCCA CAAGGGCCTTCCGGCTACCAACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGC GTGTATGTGTGAATATTGTCTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG CTGAAGGTCACTCTGGAGTGGGCAGGTGGGGGAAAGGGGCAAGGCCATGTTCTGGA GGAGGGGTTGTGACTACATTAGGGTGTATGAGCCTAGCTGGGAGGTGGATGGCCRGGTCC GGTCCCATCCAGGAAACCTCCGGCATGGCTGGGAAGTGGGGGTACTTGGTGCCGGGTCTGT 841 ATGTGTGTGTGTGTGTGTGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCT CAAGTGTGAACAAGTGGACAAGTGTCTGGGAGTGGACAAGAGATCTGTGCACCATCAGGT GTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATG ATGCCACTCATCATCAGGAGCTCTAAGGCCCCAGGTAAGTGCCAGTGACAGATAAGGGTG GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG GCAGCACAGTCAACAGCAGGTTCACTCACAGAGGGCAAAGGCCATCATCAGCTCC 421 421 481 181 541 541 601 661 781 901 196 1081 1081 1021 1021 1141 1141 901 961 1201 1201 1261 1261 1321 1321 1441 1441 1381 1381 g δğ g δ 9 δy g Ω g δλ qq g δ g QΥ qq δ ò g Óγ qq Ω qq QΥ g δλ gg QΫ́ g δ qq ò Db δy Pp

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TCTACTGAAAATAYAAAAAGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAG

181 181 GAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGGAAGGTTGTAGTGAGCCGAGATT

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GCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTCTC

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                                                                                                                                                                                                                                                                                         Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenoblotic;
11gase-based sequenced determination; drug metabolism; chromosome
CCTGGTGGGGTGGGGTGCCAGGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTA
                                                             1561 CCTGGTGGGGTGGGGTGCCAGTGTCCAGAGCCCCATTTGGTAGTGAGGCAGGTA
                                                                                                              1621 TGGGGCTAGAAAGCACTGGTGCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCGTGGTGG
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CAAAAAAAAAAAAAAAAAAAAAAAGRATTAGGCTGGGTGGTGCCTGTAGTCCCAGCTACTT

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GTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATG
                                 GAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAGGATGTTGTCACAGGCTGGGG
                                              CAAGGGCCTTCCGGCTACCAACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGC
                                                                                           GGTCCCATCCAGGAAACCTCCGGCATGGCTGGGAAGTGGGGTACTTGGTGCCGGGTCTGT
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Gaps 9 9

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Indels

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7; Mismatches

Conservative

Similarity

Best Local Sim Matches 1673;

AGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120

61

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GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATT GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCCGGTCTCTACAAAAATACAAAATT

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Best Local Similarity
Matches 1666; Conserv
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             1141 CTGAAGGTCACTCTGGAGTGGGCAGGTGGGGGTAGGGAAAGGGCAAAGGCCATGTTCTGGA 1200
                                                                                                                                              GCAGCACAGTCAACACAGCAGGTTCACTCACAGGGGAAAGGCCCATCATCAGCTCC 1500
                                                                                                                            CCTGGTGGGGGTGCCAGGTGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTA 1620
                                                                                                                                                                               TGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTGG 1680
                                                                                                                                                                                                         1621 TGGGGCTAGAAGCACTGGTGCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTGG 1680
                                       ACTGAAACCCTGGTTATCCCAGAAGGCTTTGCAGGCTTCAGGAGCTTGGAGTGGGCAGAG
                                               GGGGTGACTTCTCCGACCAGGCCCCTCCACCGGCCTACCCTGGGTAAGGGCCTGGAGCAG
                                                                                                  GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG
                                                                                                                                                                                                                                                                                                 Cytochrome P450; CYP2D6; promoter; drug metabolism; human; diagnosis; therapy; ds.
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/note= "amplification primer upf14"
                                                                                                                                                                                                                                                                                      Human cytochrome P450 CYP2D6 gene promoter region.
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/note= "sequencing primer R2"
complement (565..577)
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/note= "sequencing primer R3"
complement (968..988)
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/note= "sequencing primer F3"
1124..1143
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/note= "sequencing primer R4"
1605..1623
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/note= "sequencing primer
602..620
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/note= "sequence primer |
493..514
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The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene. The promoter region was amplified by PCR from leucocyte DNA of over 50 individuals, and sequenced. By PCR from leucocyte DNA of over 50 individuals, and sequenced. By PCR from leucocyte DNA of over 50 individuals, and sequenced. Co dentified. These were at: base 36 (base -1584 according to the concurring at an estimated frequency of approximately 20% whole population, and resulting in increased enzyme activity. Co courring at an estimated frequency of approximately 20% in the whole population, position 385 (-1235), A to G, approximately 20% frequency, neutral function; position 385 (-1235), A to G, approximately 20% frequency, neutral function; position 386 (-1000), G to A, approximately 30% frequency, unknown function; 1255 (-385), C G to A, approximately 30% frequency, unknown function; 1255 (-385), C G to A, approximately 30% frequency, unknown function; 1255 (-385), C G to A, rare, unknown function; and 129% (-322), T to C, rare, unknown function. The C to G mutation at -1584 bp is strongly associated with lower metabolic ratios, and a molecular variant polivacient or enhanced capacity for clearance of CYP2D6 substrates cuttoed or enhanced capacity for clearance of CYP2D6 substrates colliar in reutation in reutation in the CYP2D6 (antidepressant, selective serotonin reutation in the CYP2D6 cantidepressant, selective serotonin reutation in the CYP2D6 contaction between genotype and phenotype in the CYP2D6 polymorphism. Testing for the mutation will allow quentiative predictions to be made correlation between genotype and phenotype in the CYP2D6 polymorphism. Testing for the mutation will allow quentiative predictions to be made con for improving the therefore allow quentitative predictions to be made con for improving the therepower product. Testing for the mutation will allow quentiation of intermediate con in vivo drug metabolism capacity, thus providing a very potent to offer improving the presence of a worder co
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P-450
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                                                                                                                                                                                                                                                                                                                                                                                  /partial
/note= "5' region of CYP2D6 coding region"
                                   /note= "sequencing primer R5"
1650..1669
/*tag= i
/note= "amplification primer upr1669"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targets of the CYP2D6 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-EP00954.
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1620..1669
/*tag= k
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/*tag=
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                                                                           primer_bind
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0; Gaps

0; Indels

Score 1665.4; Pred. No. 0; 3; Mismatches

99.18; 99.88;

Conservative

DB 22; Length 1669;

GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATT 60

GGGAGGCAGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGCCACTGCAC 480

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Ċ,
                WPI; 2001-457734/49.
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Raimundo
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of hybridizing to CYP2D6 promoter useful for therapies using substrates of cytochrome P-450 A polynucleotide capable the optimization of drug

-; 41pp; English. Claim 1(a); Page

The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene, which includes G at position 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature). The presence of C at position -1584 bp is a marker for low enzyme activity, whereas there is strong association of G single nuclectide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates (antiarrhythmic, beta-adenergic receptor antiagonist, tricyclic antidepressant, selective serotonin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder. The novel variant forms of the CYP2D6 gene provided by the invention provide the potential for the development of a pharmacodynamic profile of drugs for a given crypto gene, and diagnostic tests for the discrimination of different alleles in human individuals, provide a very potent tool of the CYP2D6 gene production, and whose metabolism is therefore dependent on CYP2D6 activity.

Cof the CYP2D6 gene production, and whose metabolism is therefore dependent on CYP2D6 activity, and whose metabolism is therefore cerising a name of metabolism is therefore cerising a name of metabolism is therefore risting and from the CYP2D6 promoter sequence given in the Sequence is a stain and a name of the control of the cypach activity.

Sequence 1669 BP; 413 A; 376 C; 535 G; 338 T; 7 other;

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61 AGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120 120 180 180 240 300 9 9 Gaps 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATT GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC TCTACTGAAAATAYAAAAAGCTAGACGTGGTGGCACACCTGTAATCCCAGCTACTTAG GAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATT DB 22; Length 1669; .; 0 Indels 0; 99.1%; Score 1665.4; 99.8%; Pred. No. 0; ive 4; Mismatches Best Local Similarity 99.8 Matches 1665; Conservative Query Match 61 121 181 241 241 121 181 οy qq δ g qq g QQ ò Qγ δ

300 360

GCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTCTC

301 301 361 361 421

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420 480

GGGAGGCAGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGCCACTGCAC

420

1080 1140 1020 ACTGAAACCCTGGTTATCCCAGAAGGCTTTGCAGGCTTCAGGAGCTTGGAGTGGGGAGAG 1320 GGGCTGACTTCTCCGACCAGGCCCCTCCACCGGCCTACCCTGGGTAAGGGCCTGGAGCAG 1380 540 900 900 099 99 720 720 780 840 840 900 900 960 096 CTGAACAAAGGATCCTCCATAACGTTCCCACCAGATTTCTAATCAGAAACATGGAGGCCA GAAAGCAGTGGAGGAGGACRACCCTCAGGCAGGCCGGGAGGATGTTGTCACAGGCTGGGG CAAGGGCCTTCCGGCTACCAACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGC CATAGCCCGGCCAGAGCCCAGGAATGTGGGCCTGGGCTGGGAGCAGCACCTCTGGACAGGAGT GGTCCCATCCAGGAAACCTCCGGCATGGCTGGGAAGTGGGGGTACTTGGTGCCGGGTCTGT CAAGTGTGAACAAGTGGACAAGTGTCTGGGAGTGGACAAGAGATCTGTGCACCATCAGGT GTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATG ATGTGTGTGTGACTGTGTGTGTGAGAGAATGTGTGCXCTAAGTGTCAGTGTGAGTCT GTGTATGTGTGAATATTGTCTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG ATGCCACTCATCATCAGGAGCTCTAAGGCCCCAGGTAAGTGCCAGTGACAGATAAGGGTG CTGAAGGTCACTCTGGAGTGGGCAGGTGGGGGTAGGGAAAGGGCAAGGCCATGTTCTGGA GGAGGGGTTGTGACTTACGGTGTATGAGCCTAGCTGGGAGGTGGATGGCCRGGTCC GAAGCAGGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG GCAGCACAGTCAACACAGCAGGTTCACTCACAGCAGGGGCAAAGGCCATCATCAGCTCC 481 541 481 601 661 721 721 781 781 841 1021 1081 1141 901 901 961 961 1021 1201 1081 1141 1201 1261 1261 1321 1381 1501 1321 1381 1441 1441 1501 ò g a ò Db ò ò Dp ò g Op δ g δλ g ğ δ g Qγ g οy qq Qγ qq Qγ g Qγ QQ δy qq qq QQ δy δy q δy

ò g ò q

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/note "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution R88H" replace (1974, A)
                                                                                       /*tag- m
/label: PS10
/note: "Novel single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                          /note. "Known single nucleotide polymorphism (SNP); causes the amino acid substitution L91M" replace (1984, G)
                                                                                                                                                                                                                                                                                                                                                                                        /note- Novel single nucleotide polymorphism (SNP); causes the amino acid substitution H94R" replace (1997, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note" "Novel single nucleotide polymorphism (SNP); together with PS18 causes the amino acid substitution T107F" replace (2023, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel single nucleotide polymorphism (SNP); together with PS17 causes the amino acid substitution T107F"
          /note- "Known single nucleotide polymorphism (SNP); causes the amino acid substitution P34S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /notes "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution V104A" (2022, T)
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causes the amino acid substitution 1109V"
replace (2036, C)
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                                                                                                                             replace (1843, G)
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/label= PS20
/note= "Novel si
replace (2039, 7
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replace (2062,
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/label~ PS11
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/label= PS12
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Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase; antiarrhythmia; adrenoreceptor antagonist; hypertension; tricyclic antidepressant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotyping; genotyping; haplotype, genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ds.
          CCTGGTGGGGGGGGGTGCCAGGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTA 1620
                        /note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution V11M"
replace (1100, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Novel single nucleotide polymorphism (SNP)" replace (678, C)
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    causes the amino acid substitution V7M"
replace (1031, A)
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                                                                            TGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCT 1669
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                                                                                                                                                                                                                               Human CYP2D6 gene, SEQ ID NO:1 version #2.
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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replace (825,
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/*tag= ad
/label= PS25
/note= "Known single nucleotide polymorphism (SNP)"
replace (2179, C)
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/label= PS26
/note= "Novel single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                           /note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution F1201"
replace (2635, C)
                                                                                                                                                                                                                                                                                            // Anote = "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution W128R"
replace (2659, A)
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Known single nucleotide polymorphism (SNP), together with PS29 causes the amino acid substitution V1361"
                                                                                                                                                                                                                                                                                                                                               /note= "Novel single nucleotide polymorphism (SNP);
together with PS30 causes the amino acid
substitution V1361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Known single nucleotide polymorphism (SNP); causes the amino acid substitution Q151E" replace (2716, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single nucleotide polymorphism (SNP); the amino acid substitution E155K"
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/label= ps33
/note= known single nucleotide polymorphism (SNP)"
2847..3007
'note= "Novel single nucleotide polymorphism (SNP)
                                            (SNP)
                                                                                    (SNP)
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                                           nucleotide polymorphism
                                                                                  nucleotide polymorphism
                  /*tag= ab
/label= PS23
/note= "Novel single
                                                                                /note= "Novel single
                                                  replace (2118, T)
                                                                                            replace (2170, A)
                                                                                                                                                                                                              A)
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                                                                                                                                                                                                                                                                                                                                                                                 (2661, C)
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/number= 4
replace (3292, A)
           replace (2067, G)
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/label= PS24
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/label= PS27
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/label= PS30
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/label= PS32
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/number= 4
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                                                                                                                               980 AAGTGTCTGGGAGTGGACAAGAGATCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGC
                                                                                                                                                                                                   1100 GCTCTAAGGCCCCAGGTAAGTGCCAGTGACAGATAAGGGTGCTGAAGGTCACTCTGGAGT
                                                                                                                                                                                                                                                                                                        680 AACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGCCATAGCCCGGCCAGAGCCC
                                                   740 AGGAATGTGGGCTGGGAGCAGCCTCTGGACAGGAGTGGTCCCATCCAGGAAACCT
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RESULT 6 ABQ72215

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RACCCTCAGGCAGCCCGGGAGGATGTTGTCACAGGCTGGGGCAAGGGCCTTCCGGCTACC 679

Best Local Similarity 99.0 Matches 1057; Conservative

620

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Local Similarity

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/label- PS17
/note- "Novel single nucleotide polymorphism (SNP);
given as W in the specification; together
with PS18 causes the amino acid substitution
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/label: pS19
/note= "Novel single nucleotide polymorphism (SNP);
/note= "Novel single nucleotide polymorphism (SN
                                                                                                                                                                                                                                                                                                                                                                                                                   /note: "Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution R88H" replace (1974, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Novel single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution V104A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note: "Known single nucleotide polymorphism (SNP); given as M in the specification; causes the amino acid substitution L91M" replace (1984, G)
                                                                                                                              /noter "Novel single nucleotide polymorphism (SNP); given as S in the specification" replace (1843, G)
                                                                                                                                                                                                                                         /noter "Known single nucleotide polymorphism (SNP);
given as K in the specification"
1884..2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution H94R" replace (1997, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /labelo PS15
/noten "Novel single nucleotide polymorphism (SNP);
given as S in the specification"
replace (2014, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Novel single nucleotide polymorphism (SNP);
given as Y in the specification"
replace (2039, T)
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                                                                  replace (1827,
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/label~ PS10
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/label⇔ PS11
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  1181..1883
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/label: 8
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  Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22431.1; drug metabolism; detoxification; mono-oxygenase; antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertension; tricyclic antidepressant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Known single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution VIIM" replace (1100, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "Known single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution P34S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "Novel single nucleotide polymorphism (SNP); given as R in the specification"
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given as R in the specification"
replace (915, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note "Novel single nucleotide polymorphism (SNP); given as Y in the specification"
                                                                                                                              Human CYP2D6 gene, SEQ ID NO:1 version #1.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
replace (636, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "CYP2D6"
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given as
replace (776, G)
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/label~ PS9
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/product: "C
1001..1180
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ABQ72215 standard; DNA;
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1100 GCTCTAAGGCCCCCAGGTAAGTGCCAGTGACAGATAAGGGTGCTGAAGGTCACTCTGGAGT 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                    GTGTGAGAGAGAATGTGTGCCCTAAGTGTCAGTGTGAGTCTGTGTATGTGTGAATATTGT
                                                                                              ATGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATGATGCCACTCATCATCAGGA
                                      GTGTGAGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCTGTGTATGTGTATTGT
                                                                                   CTTTGTGTGGGGGATTTTCTGCRTGTGTAATCGTGTCCCTGCAAGTGTGAACAAGTGGAC
                                                                                                                              AAGTGTCTGGGAGAGACAAGAGATCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGC
                                                                                                                                                                                     1160 GGGCAGGTGGGGTAGGGAAAGGGCAAGGCCATGTTCTGGAGGAGGGGTTGTGACTACAT
                                                                                                                                                                                                                                1280 CAGAAGGCTTTGCAGGCTTCAGGAGCTTGGAGTGGGGAGAGGGGGGTGACTTCTCCGACCA
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given as R in the specification; together
with PS30 causes the amino acid substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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/note= "Known single nucleotide polymorphism (SNP);
given as Y in the specification"
                                                                                                                single nucleotide polymorphism (SNP); as R in the specification"
                                                                                                                                                                    /note= "Novel single nucleotide polymorphism (SNP);
given as K in the specification"
replace (2118, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution W128R"
                                                                                                                                                                                                                           /note= "Novel single nucleotide polymorphism (SNP); given as Y in the specification" replace (2170, A)
                                                                                                                                                                                                                                                                                /note= "Known single nucleotide polymorphism (SNP);
given as R in the specification"
replace (2179, C)
                                                                                                                                                                                                                                                                                                                                          /note= "Novel single nucleotide polymorphism (SNP);
    given as S in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Novel single nucleotide polymorphism (SNP);
given as W in the specification; causes the
amino acid substitution F1201"
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                                                                     'cons_splice= (5'site:NO, 3'site:YES)
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                                                                               replace (2062, G)
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                                                                                                                /note= "Novel sir
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/label= PS23
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Matches 1051; Conserv
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                                                                                                                                                                                                                                                                                                                                        New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5884 BP; 1259 A; 92 C; 1514 G; 3019 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 39; 24pp; English
                                                                                                                                                                                                                                                            Berlin K;
                                                                                                                29-JUN-2001; 2001WO-EP07470
                                                                                                                                                        30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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Matches 1086; Conservative
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                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
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                                       WO200202806-A2
  Homo sapiens
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3551 TAAATTTTTGTATAAAAATTAGTTAGGTGGTGGTGGGGGTATTTGTAATTTTAGTTAT 3610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, useful
abnormal
                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
          GCTCGGTGTGCTGAGAGTGTCCTGCCTGGTCTTGTGCCTGGTGGGGGTGGGGGTGCCAG
                                                                                 GTGTGTTTAGAGGAGTTTAGTTGGTAGTGAGGTAGTTATGGGGTTAGAAGTATTGGTGTT
                                                          GTGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTATGGGGCTAGAAGCACTGGTGCC
                       cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5884 BP; 1259 A; 92 C; 1514 G; 3019 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 529; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 529.
                                                                                                        1643 CCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTGG 1680
                                                                                                                      5024 TITGGITAIGATAGIGGITAITITITITITITIGGIGG
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Pred. No. 6.1
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70.6%;
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Best Local Similarity 70.6
Matches 1086; Conservative
                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytosine methylation
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                                                                                                                                                                                             standard;
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                  3716 TTTT------AAAAAAAAAATTTTGGGTTCGGTGGTGTTTGTAGTT
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                                                               GATTGCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCG
                                                                                               -----TATTTGGGCGATAGAGTAAATTTCG
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                                                                                               3671 GATCGTATTATTGTATTTT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP1181; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
                                           GTGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTATGGGGGCTAGAAGCACTGGTGCC
                                                                                                                                                                                                                                                               GAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTGGCAGCACAGTCAACACAGCAGG
                                                                                                                                                   CCCTCCACCGGCCTACCCTGGGTAAGGGCCTGGAGCAGGAAGCAGGGGCAAGAACCTCTG
                                                                                                                                     TTCACTCACAGCAGAGGGCAAAGGCCATCATCAGCTCCCTTTATAAGGGAAGGGTCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chemically pretreated gene sequence #20 strand 2.
                                                                                                                                                                                                                                                                                                   CCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTGG 1680
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ID ABK39959 standard; DNA; 5884
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01-SEP-2000; 2000DE-1043826
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CC MRP (NM_004996, NM_019900, NM_019901, NM_019902, NM_019898, NM_019899) and their complementary sequences, or a sequence (S1) chosen from 87 sequences and their complements. The chemical pretreatment c is bisulphite treatment to convert cytosines (but not methyl-cytosines) collygonoucleotide or a peptide nucleic acid (PMA)-oilgomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated bNA of can array for analysing diseases associated with the methylation state (CG) and/or detecting SNPs (single nucleotide polymorphisms) cc of the 87 sequences. The oilgomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence control of the printed specification, but was obtained in electronic cof the printed specification, but was obtained in electronic cofficial directly from MPO at
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                                                                                                                                                                                                                                                                                                                                                                               Length 5884;
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                                                                                                                                                                                                                                                                                                                                                                 Score 537.4; DB 24;
Pred. No. 8.9e-123;
                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                             32.0%;
62.4%;
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                         TGTGCYCTAAGTGTCAGTGTGAGTCTGTGTATGTGTGAATATTGTCTTTGTGTGGGTGAT
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                                                                                                               995 GACAAGAGATCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAA
                                                                                                                                                                       1055 GGTGAAGTGAAGGGACCAGGCCCATGATGCCACTCATCATCAGGGGCTCTAAGGCCCCAG
                                                                                                                                                                                                                               GTAAGTGCCAGTGACAGATAAGGGTGCTGAAGGTCACTCTGGAGTGGGCAGGTGGGGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarteriosclerotic; antianaemic; cytostatic; nootropic;
deroportective; anti-HIV; anticonvulsant; opthhalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 530.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AAATAYAAAAAGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAGGAGGCTGA 248
  epilepsy;
bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 GGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATTGCATCATT
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                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5884 BP; 1730 A; 92 C; 1381 G; 2681 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 530; 32pp + Sequence Listing; German.
myeloid leukaemia; Alzheimer's disease; AIDS; ibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 537.4; DB 24;
Pred. No. 8.9e-123;
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62.4%;
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                        cytosine methylation
                                                                                                                                                                                                            (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                               WPI; 2002-130909/17
               neurofibromatosis;
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                                                                                 WO200200928-A2.
                                                                                                                                     02-JUL-2001;
                                                                                                                                                                 30-JUN-2000;
                                                        Homo sapiens
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                                                                                                                    1055 GGTGAAGTGAAGGGACCAGGCCCATGATGCCACTCATCAGGAGCTCTAAGGCCCCCAG 1114
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                                                   AGCCCGGCCAGAGCCCAGGAA-----
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The inversion relates to detecting (M1) granilocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level in an unactivated of the expression level in an unactivated of GCA.

Also included are modulating (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for constant of GCA preferably in an inflammation in a tissue, M4 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue, M4 is useful for response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rhemmatory disease, crohn's disease, ulcerative colitis, glummatory bowel disease, crohn's disease, ulcerative colitis, virial infection, virial infection and M5 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to detecting (M1) granulocyte (GC) activation
                                                                                                                                                                                                                      Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; strile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                Human cDNA differentially expressed in granulocytic cells #140.
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                                          BP.
                                          ABK83569 standard; cDNA; 122888
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RESULT 11
ABK83569
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                                                                                                                                                                  Db 120889 GGCGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAACCCTGTC 120948
                                                                                                                                                                                                               D 120831 ATTAGGCC--GGGTGTGGTGGCTCACGTCTATAATCCCAGCACTTTGGGAGGCCGAGGCA 120888
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                                                                                                                                  Gaps
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useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087
                                                                                                                                                   1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACAAAATT
                                                                                                                                                                                                                                                                                              TCTACTGAAAATAYAAAAA---GCTAGACGTGGTGGCACACCTGTAATCCCAGCTACT
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                                                                                Sequence 122888 BP; 28761 A; 33410 C; 31919 G; 28798 T; 0 other;
                                                                                                                               3; Mismatches 116; Indels
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                                                                                                       Score 258.2; DB 2. Pred. No. 2.8e-53;
                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                       15.4%; 72.1%;
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                                                                                                                             Matches 419; Conservative
                                                                                                                    Best Local Similarity
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AAK54951 to AAK64702 encode the human immune/haematopoictic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
conclusionable may be used to produce the secreted (I), by inscrtling
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
concers and cancer metastases of haematopoietic-derived cells. AAK64703
concers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
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                                                      ID NO 33087; 3071pp + Sequence Listing; English
preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35959 BP; 8844 A; 9997 C; 9380 G; 7738 T; 0 other;
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Matches 408; Conservative
                                                        Disclosure; SEQ
useful for
                    metastasis
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Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteoporis, glucocorticoid dury-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastcoytosis, Fanconi syndrome or fibrous dysphasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention.

Note: The sequence data for this patent did not form part of the printed section, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                          Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
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                                                                                        osteoblast; stem cell differentiation; bone tissue deposition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening modulators of precursor stem cell differentiation into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoblasts, or bone tissue deposition;
(b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or
                                                                                                                                                                                                                                                                                                                 Houghton A;
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                                                             Human osteoblast differentiation related cDNA SEQ ID NO 24
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24-APR-2001; 2001US-285691P.
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(PROC ) PROCTER & GAMBLE CO.
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Best Local Similarity 68.5
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ACCCTATCTCTACTGAAAATAYAAAA---AGCTAGACGTGGTGGCACACACCTGTAATCC 229
                         290 GAGCCGAGATTGCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAA
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                                                                  CAGCTACTTAGGAGGCTGAGGAGGAAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGT
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The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
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16-MAR-2000;
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system

completed: February 11, 2003, 02:04:41 he : 990.639 secs

Search co Job time

Disclosure; SEQ ID NO 6689; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (AABB4678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

11505 11685 11686 CGAGAGGCTGAGACTGGAATTGCTTGAGCCCGGGAGGCGGAGGTTGCAGTGAGCCGAG 11745 11790 11791 CTCGAAAAAGAAAAAAAAAAATTTGTCAGGCGGGGGGCATATTCCTTTAGTCCCAG 11850 11851 CTACGCAGGAGGCTGAAGTGGGAGGAATAATTGAGCCCAGGAGGTTGAGGTTGAGGTTAG 11910 in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; haemolytic anaemia autoimmune thyroiditis, disbetes mellitus, cutofmune disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohaemius; (d) wound healing; (e) neurological diseases e.g. ccrebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. 414 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. 237 415 CTACTTGGGAGGCAGGGG------GTCCACTTGATGTCGAGACTGCAGTGAG 460 461 CCATGATCCTGCCACTGCACTCCGGCCTGGGCAACAGAGTGAGACCCTGTCTAAAGAAA 520 nucleic acids, proteins, antibodies and (ant)agonists are useful Gaps 11448 GAGTTCAAGACCAGCTTGGACAACATAGGGAGACCCCGTCTCTACAAAAAATTAGCC--61 AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 121 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC 11746 ATTGCACCATTGCAC-----TCCAGCCTAGGCAAC-AGAACAAGACTCGT 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATT 181 TCTACTGAAAATAYAAAA----AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACT 238 TAGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTTGTAGTGAGCCGAG 298 ATTGCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGT 37; Length 32169; Sequence 32169 BP; 7891 A; 8226 C; 7897 G; 8155 T; 0 other; 2; Mismatches 107; Indels 15.0%; Score 252; DB 22; 73.8%; Pred. No. 6.1e-52; 11971 ATAATAATAATAA 11988 521 AAAAATAAAGCAACATA 538 Matches 412; Conservative Local Similarity Query Match Best ρp a g g QQ g ò ŏ ò à ò οy ò ð ò ò

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NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence start: 3

High quality sequence stop: 536.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                    BE792565
AQ057239
AL04489
AQ897694
AQ162975
AQ11380
AG019426
AU158859
AQ158859
                                                                                                                                                                           AG031448
BQ028890
AQ386729
AV699423
BF376376
AQ599255
AG094205
                                                                                                                                                                                                                                                                                                                            AQ588913
BG476945
BG75059
BG7010345
BG710345
BG710345
AG185174
AQ412029
AL135698
BM917683
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AG094775
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KEYWORDS
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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BQ067695
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    BQ067695 AGENCOURT
AQ424894 CITBI-EI-
BI910844 603068871
AQ428350 CITBI-EI-
T06700 ESTQ4589 FE
AQ061135 CIT-HSP-2
                                                                                           20:51:09; Search time 4846.73 Seconds (without alignments) 5613.764 Million cell updates/sec
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               5.1.3
Compugen Ltd
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               version 5
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Maximum Match 100%
Listing first 45 summaries
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AQ424894
BI910844
AQ428360
T06700
AQ061135
                                                                   nucleic search, using sw model
                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
               GenCore
Copyright (c) 1993
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em_gss_inv:*
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seq length: 200000000
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em_estro:*
em_htc:*
ep_bestl:*
gb_est2:*
gb_est3:*
gb_est4:*
gb_est4:*
em_est6iu:*
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Match
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26.0
24.7
21.0
19.2
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462.4 436.6 414.8 352 322.6 245.6

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Score

Result š. and

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In Unpublished (1997)
Other_GSSs: CTTBI-E1-2576P11.TR
Conteart: Shaying Zhao, William Nierman, Mark Adams
Conteart: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end Search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sass 1 to 449)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready map Building
                                                                                                                                                                                                                                                                                                                                                                                                                               61 TGGGATTGGGTGCGTCGTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTGGGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTCTCCAA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACAAAATTAGC
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0
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inc 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 436.6;
Pred. No. 5.2e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 449
Acganism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCAGGGGTCCACTTGATGTCGAGACT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.0%;
Best Local Similarity 97.8%;
Matches 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
                                                                                                                                                                                                                                                                                                                                                         source
            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                        REFERENCE
                                                                      AUTHORS
                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
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                                                                                                    TITLE
                                                                                                                                              COMMENT
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1. .1180
/organism="Homo sapiens"
/dorganism="Homo sapiens"
/dorganism="Homo sapiens"
/dorganism="Mixecn:9806"
/clone_lib="NIH_MGC_121"
/lab_host="Mixecn:9606"
/flone_lib="NIH_MGC_121"
/lab_host="Mixecn:9607"
/lab_host="Mixecn:9607"
/note="CoRV (destroyed); RNA source anonymous pool of setal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITBI-E1-2576P11.TF CITBI-E1 Homo sapiens genomic clone 2576P11, DNA sequence.
A0424894.1 GI:4498160
GSS.
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                                                                                                                                                                                                                                                                                                                      29; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 CTGGGATCCACGTGACAGCTTTGAGGCTCACTGGGAGGAGCAGCCTCTGGACAGGAGAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    786 CATCCAGGAAACCTCCGGCATGGCTGGGAAGTGGGGTACTTGGTGCCGGGTCTGTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGTGACTGGTGTGTGAGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCTGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 462.4; DB 14; Length 1180;
Pred. No. 3.9e-61;
3; Mismatches 24; Indels 29;
                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1086 ACTCATCAGGAGCTCTAAGGCCCCAGG 1115
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                                                                                                                                                                                                                                                                                      27.5%;
90.2%;
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Matches 514; Conservative
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      source
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AQ428360 364 bp DNA linear GSS 24-MAR-1999
CITBI-E1-2576K5.TF CITBI-E1 Homo sapiens genomic clone 2576K5, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
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t
     168 CAAGGGCCTTCCGGCTACCAACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                      4 TTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATTAGC
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                                                                                                                                                             780 IGGICCCAICCAGGAAACCICCGGCAIGGCIGGGAAGIGGGGIACIIG 827
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3.8e-44;
cches 7;
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/note="Vector: pBeloBAC11;
CalTech Human BAC Library D
82 c 98 g 78 t
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1. 364
// Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2576K5"
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AQ428360.1 GI:4496126
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97.5%;
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Matches 355; Conservative
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Class: BAC ends
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                           B1910844 186 bp mRNA linear EST 16-OCT-2001 603068871F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217977 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note:"Vector: DCMV-SPORT6; Site_1: Not1; Site_2: ECCRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (ECCRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NH-MGC Library."
                                                                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
MIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can hour through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11547 row: m column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGGCAGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGCCACTGCACT
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Pred. No. 7.4e-54;
1; Mismatches 18;
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/db_xref="taxon:9606"
/clone="ImAGE:5217977"
/clone=lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_hoste"DH108"
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High quality sequence stop: 432.
Location/Qualiflers
                                                                         mRNA sequence.
BI910844
BI910844.1 GI:16174292
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95.5%;
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Best Local Similarity 95.5
Matches 447; Conservative
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BI910844/C
                                                   DEFINITION
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AUTHORS
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1. 631
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CIT-HSP"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
                                                                                                                                                                       AQ061135
AQ061135.1 GI:3363047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.4%;
Matches 414; Conservative 3
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ORIGIN
                                                                                                                                                                       ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                                                    REF'ERENCE
                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .332

/organism="Homo sapiens"

/db_xref="ArCc (inhost):83354"

/db_xref="taxon:9606"

/clone="HFBDX16"

/clone="HFBDX16"

/clone="HFBDX16"

/clone="Lib="Fetal brain, Stratagene (cat#936206)"

/note="Vector: LambdaZAP-II; 17-18 wk gestation, female; oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average inser size."
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        female;
                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 382)
Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
3.400 expressed sequence tags identify diversity of transcripts from human brain
GCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATTGCA 303
            141 GAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATCTCTACTGAAAATAYAAAAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATTGCATTGCATAGCACAATGGAGG 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 AACTTGGAAGAACCSGGTCTCTACAAAAAAA-CAAAATTAGCTGGGATTGGGTGCGGTG 80
                                                   TCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.2%; Score 322.6; DB 14; Length 382; 97.9%; Pred. No. 1.1e-39; Live 2; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 4, 256-267 (1993)
93364420
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13-21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 3018699423
Email: mdadams@tigr.org
                                                                                                                                                                                                                 EST04589 Fetal brain,
clone HFBDX16 similar
                                                                                                                                                                                                                                                         T06700.1 GI:317849
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                                                                                                          364 AAAA 367
                                                                                                                                   361 TATA 364
                                                                                                                                                                                                       T06700
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hes 333;
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TITLE
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T06700/c
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KEYWORDS
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1. (Jadams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

Unpublished (1998)

Other_GSSs: CIT-HSP-2348E15.TR

Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                         AQ061135 631 bp DNA linear GSS 31-JUL-1998 CIT-HSP-2348E15.TF CIT-HSP HOMO Sapiens genomic clone 2348E15, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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                                   41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3; Mismatches 112; Indels
                                                                       321 GGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTCTC 360
                                                                                                     GAGCCACCAGCCTGGGCNACAAGAGGAAATCTCCGTCTC
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us-09-942-310-2.rst

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Homo sapiens
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AQ635492/c
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 10-NOV-1999
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HS_3135_A2_A11_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate 3135 Col-22 Row-A, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High Throughput Sequencing Center
University of Washington
University of Washington
University of Washington
University of Washington
Tol. (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
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                                                                                                                                                                                                                                                   CAGTGAGCCATGATCCTGCCACTGCACTCCGGCCTGGGCAACAGAGTGAGACCCTGTCTA 513
                                                                                                                          407
                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clones"Plate 3135 Col=22 Row=A"
/clone_lib="CIT Approved Human Genomic Sperm Library
                                                                                                                                                                                                                                                                                  139 CAGTGAGCCAAGATCACATGACTGCACTCCAGCCTGGGCAACAGAGTTAGACTCTGTCCC 80
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              CGTCTCCAAAAAAAAAAAAAAAAAAAAAGRATTAGGCTGGGTGG------TGCCTGTA
                                                                                                                                                         CATCTCAAAAAAAAAAAAAAAAAAAAAAATTAGCGGAGCGTGGTGCCTGCTGTA
                                                                                                                                                                                      GTCCCAGCTACTTGGGAGGCAGGGG-------GTCCACTTGATGTCGAGACTG
                                                                                                                                                                                                                      GTCCCAGCTATTTGGGAGGCTGAGGCATGAGAATCGCTTGAACCCAGGAGGCAGAGGTTG
ACTTAGGAGGCTGAGGCAGGAGATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCC
                                                            GAGATTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 3.6e-28;
2; Mismatches 126; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC end Web Server: http://www.htsc.washington.edu
Plate: 3135 row: A column: 22
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E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                               514 AAGAAAAAAAAATAAAGCAACATATCCTGAA 545
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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AQ897828.1 GI:6353934
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14.6%;
Best Local Similarity 71.2%;
Matches 423; Conservative 2
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MEDLINE
COMMENT
235
                                                            295
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AQ635492 669 bp DNA linear GSS 17-JUN-1999
RPCI-11-490H22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-490H22
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
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Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
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                                                                                                                                                                                                                            416
                                                                                                                                                                      487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 GAGGCTGAGGCAGGAGAATTACTTGAACCTGGGAGGCGGAGGTTGTGGTGAGCTGAGATT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAAAATCTCCGTCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AAAAAAAAAAAAAAAAAAAAATTAGCCAGGCGTGGCAAGCACCTGTATTCCCAGTT 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A-----TGATCCTGCCACTGCACTCCGGCCTGGGCAACAGAGTGAGACCCTGTCTAAAG 516
                                                                                                               CTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTGGG 122
                           140 GTGATTGTGATCTTGCCACTGCACTTCAGCGTGGGAGAGCAGAGGAAGCACACATCTCATT
ATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATTAG
                                                                                                                                                                                                                                                                                                                                               183 TACTGAAAATAYAAAA--AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 AAAAAAAAAAAAGCAACATATCCTGAACAAAGGATCCTCCATAACGTTCCCA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAAAAAAAAAAAAAAAAAAAAGAGAGAGAGAAAGATACAGCAGCTTCCCA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , DNA sequence.
AQ635492
AQ635492.1 GI:5098127
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us-09-942-310-2.rst

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Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,Z., and Han,Z.
Homo sapiens cDNA HTF clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                               Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV730440 AV730440 HTF Homo sapiens cDNA clone HTFAWE01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TT----GGCCGGGCGGGGGGCTCTACCCACCCACACTTTGGGAGCCCAGGGCG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TCTACTGAAAATAYAAAA---AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCAGCTACTTGGGAGGC--AGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 TAGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCCATCTACTCAGGAGACTGAGGCAGAACCCAGGAGGTGGAGACTGCACTCAGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 235.4; DB 10;
Pred. No. 1.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Hypothalamus"
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/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                              1. .577
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 g
                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="HTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%;
72.0%;
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Matches 385; Conservative
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AV730440
LOCUS
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      AUTHORS
                                                                                                                 COURNAL
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                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                             TITLE
                                                                                                                                     COMMENT
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AV732057 GI:10849602
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 577)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 GA-GGTGGGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 GAGCCGAGATTGCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                              Length 669;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                            Score 241; DB 17;
Pred. No. 1.9e-27;
3; Mismatches 118;
                                          Location/Qualifiers
1..669
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                                                                                                                                                                                                                                                                                                                                              14.3%;
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Best Local Similarity 72.25
Matches 405; Conservative
primer: T7
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                                            FEATURES
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 812)

NiH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CON Library Preparation: Ling Hong/Rubin Laboratory

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE792565 812 bp mRNA 11near EST 20-SEP-2000 601585351F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939468 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 CA----GGTGGGGTGCGGTAGCTCACACTCTAATCCCAGCAATTTGGGAGGCTGAAGTA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 TCTGCTAAAAATAGAAAAATCAGCTGGGCATGGTGGCGTGTGCCTGTAATCCCAGGTACT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTACTGAAAATAXAAA---AGCTAGACGTGGTGGCACACCACCTGTAATCCCAGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
13.9%; Score 234; DB 12; 70.9%; Pred. No. 2e-26; tive 2; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 683.
Location/Qualifiers
                                                                                                                                                               BE792565.1 GI:10213763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .812
                                                                                                                                  mRNA sequence.
BE792565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Sim
Matches 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                               KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                 LOCUS
                 470
                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                               REFERENCE
                                                                  RESULT 11
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/dev_stage~"Adult"
/lab_hoste"SOLR"
/note."Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120
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                                                                                                                                                                                                                                                                                                                           Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 234.6; DB 10
Pred. No. 1.8e-26;
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/db_xref⇔"taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="HTFAWE01"
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AV730440
AV730440.1 GI:10839861
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Best Local Similarity 72.7%;
Matches 380; Conservative
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Best Local S
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AQ057239 660 bp DNA linear GSS 30-JUL-1998
CIT-HSP-2340D14.TR CIT-HSP Homo sapiens genomic clone 2340D14, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC
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1 (bases 1 to 660)

Adams, M. D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                 417
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ATTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGT 357
                                                                                                                                     --- GTCCACTTGATGTCGAGACTGCAGTGAGCC 462
                                                                                                                                                                                                                  /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                    463 ATGATCCTGCCACTGCACTCCGGCCTGGGCAACAGAGTGAGACCCTGTCTAAAGAAAAA
                                                                DB 17; Length 660;
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Other GSSs: CIT-HSP-2340D14.TF
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0208
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/db_xref="taxon:9606"
/clone="2340D14"
/clone_lib="CIT-HSP"
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AQ057239.1 GI:3353765
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Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 646)
Ansorge, W., Benes, V., Krieger, S., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the 3 sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s. Wiemann@dkfz- heidelberg.de, sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120
590 GGATTCAAGACCAGCCTGAGCAACATGACAAAAACCCCATCTCTACAAAAAATACAAAAT 531
                                                 121 GGIGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC 180
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DKFZp4341202_s1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp4341202 3', mRNA sequence.
                                                                                                             181 TCTACTGAAAATAYAAAA---AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACT
                                                                                                                                                                                                                                                                                      298 ATTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGT
                                                                                                                                                                                                                                                                                                            193 CCCAGGCAGCTGAGATGAGAAGATTGCTTGAGCCCAGGAGGCGAAGGCTGCAGTGAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST (Ansorge, Benes, et al.)
Unpublished (1999)
Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL044489.1 GI:5432707
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AQ897694.1 GI:6353980
GSS.
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                                                                                                                                         39;
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                ; Site_1: NotI; Site_2:
205 t
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                                                                                                                                         Indels
                                                                                                                Length
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                                                             /noter"Vector: pSport1;
168 c 136 g 20
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
plate: 3135 row: C column: 24
Seq primer: T7
Class: BAC ends
High quality sequence stop: 738.
Location/Qualifiers
in. 738
Loration/Qualifiers
Loration/Qualifiers
Lorganlsm-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 ACTAGAGACCAGCCTGGGCAACATAGCAAGACCTCATCTTTAGAAATAATTTAAA ---AA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GCTACTTGGGAGGCAGGGGGTCCACTTGATGTCGAGACTGCAGTGAGC--- 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GAGGCTGAGGCAGGAGATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
/note="organ: sperm; Vector: pBeloBAC11; BAC 15-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 225.8; DB 17; Length Pred. No. 3.6e-25; 1; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.4
Best Local Similarity 69.0
Matches 412; Conservative
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AV762975 MDS Homo sapiens cDNA clone MDSCKG10 5', mRNA sequence.
AV762975
                                                                                              Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)

Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,

Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng, Li,N,Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,

Homo sapiens cDNA MDS clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgechgc.Sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB" a 143 c 170 g 110 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 225.6; DB 10; Length 593; ilarity 71.0%; Pred. No. 4.3e-25; Conservative 3; Mismatches 117; Indels 35;
                                                                                                                                                                                                                                                                                                                                                           Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .593
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MDSCKG10"
                                               AV762975.1 GI:10920823
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Best Local Similarity
Matches 379; Conserv
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COMMENT
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AUTHORS
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Search completed: February 11, 2003, 03:31:02 Job time : 4853.73 secs

Appl Appl Appli Appli Appli Appli

Sequence 8, Sequence 8, Sequence 8, Sequence 42, Sequence 10, Sequence 11, Sequence 2, Sequence 3, Sequence 33, Sequence 43, Sequence 43, Sequence 57, Sequence 5, Sequence 6, Sequence 6,

Appli Appli Appl Appl Appl

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APPLICANT: Staels, Bart
APPLICANT: Croston, Glean E.
APPLICANT: Croston, Glean G.
TITLE OF INVENTION: MODULATORS OF OD GENE AND
TITLE OF INVENTION: SCREENING METHODS THEREFOR
CORRESPONDENCE ADDRESS:
US-09-608-285A-8
US-09-350-836B-8
US-09-608-285A-8
US-09-608-285A-59
US-09-608-285A-59
US-09-608-285A-59
US-09-026-033-1
US-09-026-033-1
US-09-026-033-2
US-09-035-07-033-2
US-08-857-808-87-033-2
US-09-951-896-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: STORAGE
MEDIUM TYPE: STORAGE
COMPUTER: IBW Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEED for Windows Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,100B
FILING DATE: March 19, 1996
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,584
FILING DATE: October 30, 1995
APPLICATION NUMBER: 08/510,584
FILING DATE: AUGUST 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: March 2, 1995
ATTORATION NUMBER: 08/418,096
FILING DATE: March 2, 1995
ATTORATION NUMBER: 08/418,096
FILING DATE: MARCH 20, 1995
ATTORATION: MARCH 20, 1995
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                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08618100B
Patent No. 6088976
GENERAL INFORMATION:
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,327
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NE: (213) 489-1600
: (213) 955-0440
67-3510
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                                                                                                                                                                                                                                                                                                                                                                            Auwerx, Johan
de Vos, Piet
Staels, Bart
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REGISTRATION NUMBER: 32
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California
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STATE: Californi
COUNTRY: U.S.A.
ZIP: 90071-2066
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APPLICANT:
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Sequence 3, Appli
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Sequence 1, Al
Sequence 20, A
Sequence 21, A
Sequence 22, A
Sequence 5, Al
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Sequence 1, Al
Sequence 10,
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                                                                                                                                                                                                                                                           882724
                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/RB_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-068-945A-1

US-08-44-2805-1

US-09-87-180-3

US-09-122-1268-1

US-08-724-394A-21

US-08-724-394A-21

US-08-724-394A-21
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US-09-305-384-1
US-09-305-284-7
US-07-914-281-5
US-08-393-246-5
US-08-696-731-5
US-08-696-731-5
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-09-791-211-10
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Maximum Match 100%
Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
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1680
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Match Length
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Maximum DB s
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RESULT 3
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Patent No. 6387677

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001158

CURRENT APPLICATION NUMBER: US/09/800,960

CURRENT FILING DATE: 201-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 62804
                                                                                                                                                                                                      AGCIGGGATIGGGIGCGGIGGCTCAIGCCIATAAICCCAGCACTIIGGGAGCCIGAGGIG 120
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                                                                                                                                                                 35;
                                                                                                                                        Length 10684;
                                                                                                                                  Score 250; DB 3; Length 10
Pred. No. 4.4e-57;
3; Mismatches 118; Indels
                                                               MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Sequence between exon 1 and exon ent No. 6068976
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14.9%;
Best Local Similarity 72.1%;
Matches 404; Conservative
              . 10684 base pairs
nucleic acid
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SEQUENCE CHARACTERISTICS
                                         single
                                                     linear
                                      STRANDEDNESS:
TOPOLOGY: lin
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                                                                                            ; Patent No. 606
US-08-618-100B-3
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                                                                                                14.5%; Score 244.2; DB 4; Length 73.3%; Pred. No. 3.5e-55; Live 3; Mismatches 101; Indels
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New DNA Sequences
58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08068945A Patent No. 5616483 GENERAL INFORMATION:
                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Garisson, Peter APPLICANT: Enerback, Sven APPLICANT: Hansson, Lennart APPLICANT: Lidberg, Ulf APPLICANT: Nilsson, Jeanette APPLICANT: Tornell, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGCTACTTGGGAGGCAGGGG
| NAME/KEY: misc_feature
| LOCATION: (1)...(62804)
| OTHER INFORMATION: n = A,T,C
US-09-800-960-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bjursell, Gunnar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Case
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                                                                                                                                      Matches 407; Conservative
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COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
                                                                                                                    Similarity
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..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
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join[1722..1727, 4071..4221, 4307..4429, 4707

..4904, 6193..6323, 6501..6608, 6751..6868, 8335

..851, 8719..8922, 10124..10321, 10650..11391)

NMATION: /EC_number= 3.1.1.1

NMATION: /product= "Bile Salt-Stimulated Lipase"
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-052
TELECOMMUNICATION INFORMATION:
TELECHONE: (212)819-8783
TELEFAX: (212)854-8113
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPPLOGY: 110000
                                                                                     PAPLICATION NUMBER: US/08/068,945A
FILING DATE: 27-MAY-1993
CLASSIPICATION: 435
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-7UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-7UN-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-7UL-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 1993
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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LOCATION: join(1722
LOCATION: ..4904, 6
LOCATION: ..8521, 8'
COTHER INFORMATION: ,
OTHER INFORMATION: ,
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                                                                                                                                                                                                                                                                                        Score 233.6; DB 1;
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Patent No. 5716817
GENERAL INFORMATION:
APPLICANT: Bjursell, Gunnar
APPLICANT: Carlsson, Peter
APPLICANT: Enerback, Sven
                                                                                                                                                                                                                                                                                     Query Match 13.9%;
Best Local Similarity 71.3%;
Matches 388; Conservative
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10650..11490
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10124..10321
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FEATURE:
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US-08-068-945A-1
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US-08-442-806-1
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join(1653..1727, 4071..4221, 4307..4429, 4707
..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
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LOCATION: join(1722.1727, 4071..4221, 4307..4429, 4707
LOCATION: .4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: .8521..8719..8922, 10124..10321, 10650..11391)
OTHER INFORMATION: /Eq.number= 3.1.1.1.
                                                                                                                                                                                                                                                                  COUNTRY: United States
ZIP: 10036-2787
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,806
                                                                        Genomic DNA Sequences
Encoding Human BSSL/CEL
58
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SLENCE, NUMBER: 35,372
REGENCE/DOCKET NUMBER: 31,373
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEPHONE: (212)814-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
ATRANDEDRESS: double
                                                                                                                                                                         ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,945
FILING DATE: 27-MAY-1993
CLASSIFICATION: 435
                                                   Jeanette
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TISSUE TYPE: Mammary gland
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ORIGINAL SOURCE:
         Lennart
                                                                 APPLICANT: Tornell, Jan.
TITLE OF INVENTION: GenCTITLE OF INVENTION: EncoUNDER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS: ADDRESSEE: White & Cag
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FEATURE:
NAME/KEY: TATA_signal
                         Lidberg, Nilsson,
      Hansson,
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5344 TCTCTACTAAAAATACAAAATTAGCCAGGCGTGGTGGCGCTTGCCTGTAATCCCAGCTAC 5403
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Pred. No. 1.1e-52;
3; Mismatches 117; Indels
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Best Local Similarity 71.3%;
Matches 388; Conservative
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12299 AAGAAAAAACC 12310

5570 GCTACCTGGGAGGCAGAGGTGGAAGGATCGCTTGAGCCCAGGGGTTCAAAGCTGCAGTGA 5629

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3816 CTACTCGGGAGGCTGAGGCAGGAGAATTGCTGGAACCCAGGTGGCGAAGGTTGCAGTGAG 3757
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FITLE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 AAAAAAAAAATAAAGCAACATATCCTGAACAAAGGATCCTCCATAAC
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Pred. No. 1.2e-51;
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                                     US-09-122-126B-1/c
; Sequence 1, Application US/09122126B
; Patent No. 6451575
                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%;
70.0%;
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US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                      TYPE: DNA
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APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBENCE: CLOOIL83
CURRENT APPLICATION NUMBER: US/09/817,180
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PSEXESQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15297
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                   5630 GCCGTGGTCGTGCCACTGCACTCCAGCCTGGGCGAAAGAGTGAGGCCCCATCTCAAAAAT 5689
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460 GCCATGATCCTGCCACTGCACTCCGGCCTGGGCAACAGAGTGAGGACCCTGTCTAAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TCTACTGAAAATAYAAAA---AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACT
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Pred. No. 2.1e-52;
3; Mismatches 145;
                                                                                                                                                                                                       Sequence 3, Application US/09817180 Patent No. 6340584
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69.0%;
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Matches 381; Conservative
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; ORGANISM: Human
US-09-817-180-3
                                                                                                             5690 AAGA 5693
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-09-817-180-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Megabase Transcript Map: No. 587 TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                            409 TCCCAGCTACTTGGGAGGCAGGGGGT------
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STREET: Two Embarcadero Center, 8th
CITY: San Francisco
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....bER: US/08/724,394A
01-OCT-1996
71: 536
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COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
``WDUTER: IBM PC COMPATIBLE
'`VSTEM: PC-DOS/MS-DOS
'`STEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08724394A; Patent No. 5872237; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 206222 TTAAAATCTTAAAAAAGAAA 206242
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APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                     514 AAGAAAAAAAATAAAGCAA 534
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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SEQUENCE CHARACTERISTICS:
TRNGTH: 246240 base pairs
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Kronmal, Gregory
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not relevant
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LOCATION: 1..246240
OTHER INFORMATION: /not
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APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS
ADDRESSE: TOWNSEND
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STRANDEDNESS: not 1
            Db 205996 TCCCGCCATTGCA---
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Best Local Similarity
Matches 392; Conserv
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US-08-724-394A-21
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC
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                                                                                                                                                                                                                                      TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 215.4; DB 2; 69.9%; Pred. No. 3.3e-47;
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches 119;
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTATION OF THE STATE OF THE
                                                         Gregory S.
                                                                                                                                                   Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
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TOPOLOGY: not relevant
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LENGTH: 246240 base pairs
                                                                                   Lauer, Peter M.
Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                               : Feder, John N.
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                                                            Kronmal,
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Matches 392; Conserv
GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                         Db 206162 CCATGAGCCATCATGGTGCCACTGTACTCCAGTCTAGGAAAAAATAAACATTAAAATT 206221
206042 TCAAAAAAAAAAAAAAAAAAAAAAAAAAATTAGTCAGGTGTGGTTGTGCACACCTGTAG 205101
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                                                           ----CCACTTGATGTCGAGACTG
                                                                                                                                                          454 CAGTGAGCCATGATCCTGCCACTGCACTCCGGCCTGGGCAACAGAGTGAGACCCTGTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                         D 205936 GGGAGGCTGAGGAGAGAATTGCTTGAACCTGGGAGGTAGAGGTTGCGGTGAGCCGAGA 205995
                                               Db 205702 GAATTCAAGACCAGCCTGGACAACACAGGGAAAGCCCATCTCTACAAAATATACAAAATT 205761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 206162 CCATGAGCCATCATGGTGCCACTGTACTCCAGTCTAGGAAAAAATAAAATTAAAAATT 206221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 206102 TCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCGGGGAAGTGTAGGCTA 206161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 TTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTC 358
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                                                                                           61 AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120
                                                                                                                                                                                                                                                                                  181 TCTACTGAAAATAYAAAA--AGCTAGACGTGGTGGCACACCTGTAATCCCAGCTACTT 238
GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATTACAAAATT
                                                                                                                                                                                       121 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC
                                                                                                                                                                                                                                                                                                                                                                                239 AGGAGGCTGAGGCAGGAGTTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGA
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APPLICANT: Feder, John N.
APPLICANT: Feder M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger Transcript Map: No. 5872237el
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FLING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: TWO Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
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US-08-724-394A-22
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Db 205702 GAATTCAAGACCAGCCTGGACAACACAGGGAAAGCCCATCTTACAAATATACAAATT 205761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206102 rcccascracrrsssasscrsassrssassassarcacrrsascccssssaasrsrasscra 206161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 TTGCATCATTGCACAATGGAGGGGGGGCCACCAGGGCAACAAGAGGAAATCTCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 215.4; DB 2;
Pred. No. 3.3e-47;
                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note "HLA-H.CONTIG"
US-08-724-394A-22
                                                                          017957-000100
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                  NAME: FILTS, Renee A.
REGISTRATION UNDRER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEFAM: 415-576-0200
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24624 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 AAGAAAAAAAAATAAAGCAA 534
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ATTORNEY/AGENT INFORMATION:
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E: cDNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                     TOPOLOGY: no
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-305-384-5
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6679
                                                                                      US-09-305-384-1
                                SEQ ID NO 1
                                                                                                                  Query Match
                                                LENGTH:
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TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY CHIER REPERBENCE: 07236/017001
CURRENT APPLICATION NUMBER: 08/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
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Patent No. 624218
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Treco, Douglas A.
APPLICANT: Belden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/017001
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
                                                                                                                                                                                                                                                                                                                 --TATGGCGGGCATGGTGGCTCACGTCTGTAATCCCTGAACTTTGGGACATCAGGCAA 132
                                                                                                                                                                                                                                                                                                                                                                       253 CAGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAG 312
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                                                                                                                                                                                              DB 4; Length 6235;
                                                                                                                                                                                          12.8%; Score 215.2; DB 4;
llarity 68.5%; Pred. No. 7.2e-48;
Conservative 2; Mismatches 140;
                                                                                           SOFTWARE: FastSEO for Windows Version 3.0
SEQ ID NO 5
LENGTH: 6235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 AAAATAAAGCAACATA 538
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                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                          Best Local Sim
Matches 381;
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                                                                                                                                       TYPE: DNA
                                                                                                                                                                                            Query Match
Best Local 3
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62 GCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTGG 121
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                                                                                                                                                                                                                                                                                                                       94 --TATGGCCGGCCATGGTGGCTCACGTCTGTAATCCCTGAACTTTGGGACATCAAGGCAA
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                                                                                                                                                     Length 6679;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Cancilla, Michael R.
ITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                      2; Mismatches 140;
                                                                                                                                                     DB 4;
                                                                                                                                                                       .4e-48:
                                                                                                                                                   Score 215.2;
Pred. No. 7.46
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-078-284-7/c; Sequence 7, Application US/09078294; Patent No. 6265211
                                                                                                                                                12.8%;
68.5%;
                                                                                                                                                                   Best Local Similarity 68.5
Matches 381; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 11811
; TYPE: DNA
; ORGANISM: BAC-F2 contig
US-09-078-294-7
                                                                        TYPE: DNA ORGANISM: Homo sapiens
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4017 TCCAAAAAAAAATAAATAAATTAGCTTGGCATGGTGGCACATGTCTGTGGTCTCAGCTA 3958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGCIGGGATIGGGIGCGGIGCCTCAIGCCTAIAAICCCAGCAGTIIGGGAGCCIGAGGIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 214.6;
Pred. No. 1.26
                                                                                                  NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEFAX: (703)486-2347
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
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; Sequence 5, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%;
68.0%;
                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                     8174 base pairs
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                           APPLICATION NUMBER: US
FILING DATE: 19920720
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                                                                                                                                                                                                                                                                                                      NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                  unknown
                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 HOLECULE TYPE:
ANTI-SENSE: NO
US-07-914-281-5
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                                                                                                                                                                                                                                                                                       LENGTH:
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TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GIYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                                                                        6073 AAATAGTAAAAACAAAACAAAACAAAACCCTGGCTGTGCATGGTGGCTCACCCCTGTAAT 6014
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                                                                                 2 AATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAA----TACAAA 57
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                                                                                                                                                                                                                                                                                                                                                                                                          234 TACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGC
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12.8%; Score 215; DB 4; Length 11811; 66.1%; Pred. No. 1.1e-47; 1ve 2; Mismatches 167; Indels 37.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: VISIAL COUNTRY: U.S.A.
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Patent No. 5324663
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-
SOFTWARE: PALENTIN Release #
                                           Conservative
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                      Similarity
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4017 TCCAAAAAAAAAATAAATTAGCTTGGCATGGTGGCACATGTCTGTGGTCTCAGCTA 3958
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            418 CTTGGGAGGCAGGGGGTCCACTTGATGTCGAGACTGCAGTGAGCCATGATCCTGCC----
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SOFTWARE: PAT-entin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
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Pred. No. 1.2e-47;
!; Mismatches 155;
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ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08525058A
; Patent No. S770420
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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68.0%;
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Matches 379; Conservative
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EDNESS: double
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US-08-525-058A-5/c
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US-08-525-058A-5
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                   OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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     METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOM
                                                                                                         OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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1755 Jefferson Davis Highway, Fourth Floor
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Pred. No. 1.2e-47;
1; Mismatches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lavalleye, Jean-Paul M. P. REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-WAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,24
                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
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68.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 68.09
Matches 379; Conservative
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EDNESS: unknown
TITLE OF INVENTION: OF
TITLE OF INVENTION: OF
TITLE OF INVENTION: GLY
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                          CITY: Arlington STATE: Virginia
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STRANDEDNESS:
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                                                                                                          ADDRESSEE:
                                                                                                                         ADDRESSEE:
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TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS: 5 4362 GAGTICAAGAICAGCCIGGGCAACAGAGCA-CICITACAAAAAATTTAAAATTAGCIT 4304 61 AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 120 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAAAAATT 60 :: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. 1755 Jefferson Davis Highway, Fourth Floor Length 8174; Indels g

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                                             TTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTC
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Search completed: February 11, 2003, 05:40:53 Job time : 1147.66 secs

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Sequence 2362, Ap
Sequence 1157, Ap
Sequence 1157, Ap
Sequence 2209, App
Sequence 292, App
Sequence 293, App
Sequence 36, Appl
Sequence 3, Appl
Sequence 1142, Ap
Sequence 1142, Ap
Sequence 237, App
Sequence 2385, Ap
                                                                              February 11, 2003, 03:31:30 ; Search time 152.485 Seconds
(without alignments)
5222.300 Million cell updates/sec
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                                                                                                                                                                    l gaattcaagaccagcctgga......catcttcctgctcctggtgg 1680
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                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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5.1.3
Compugen Ltd.
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US-10-096-960-3

US-09-880-107-2362

US-09-764-869-2209

US-09-954-531-180

US-09-952-832-119

US-09-962-832-119

US-09-962-832-119

US-09-962-832-119

US-09-962-832-119

US-09-764-877-2903

US-09-880-107-1542

US-09-880-107-1542

US-09-764-864-1661

US-09-764-855-227

US-09-764-857-2275

US-09-764-852-227
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                                                                                                                                                                                                                                      408267 seqs, 237001491 residues
 GenCore version
Copyright (c) 1993 - 2003
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                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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14.5 62804
14.3 21470
14.2 65608
14.2 65608
14.1 64608
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13.9 465237
13.8 110597
13.8 5386
13.8 5386
13.7 16086
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Match
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10:
110:
113:
14:
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2237.8
2237.6
2237.6
2232.8
2332.4
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230.8
2230.8
2230.8
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Maximum DB
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GENERAL INCOMATION:
APPLICANT: YAN, Xianghe et al.
APPLICANT: YAN, Xianghe et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFRENCE: CLOOL124
CURRENT APPLICATION NUMBER: US/09/835,081
KUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0 Sequence 1134, App Sequence 1134, Ap Sequence 2645, Ap Sequence 370, App Sequence 193, App Sequence 194, App Sequence 3, Appl1
Sequence 71, Appl1
Sequence 71, Appl
Sequence 351, App
Sequence 351, App 5 22435 Gaps 9 1 GAATTCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACAAAATT AGCTGGGATTGGGTGCGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCCTGAGGTG 37; Length 57130; Indels Score 249; DB 10; Pred. No. 7.2e-46; 3; Mismatches 113; US-10-161-510-1 US-09-764-904-71 US-09-764-904-71 US-10-174-590-351 US-10-175-737-351 US-10-175-737-351 US-10-175-737-351 US-10-175-738-351 US-10-175-738-351 US-10-175-738-351 US-10-175-738-351 US-10-176-757-351 US-10-176-757-351 US-10-176-757-351 US-10-176-757-351 US-10-176-757-351 US-10-180-552-351 US-09-764-80-1134 ALIGNMENTS Sequence 3, Application US/09835081 Patent No. US20020151020A1 14.88; 72.48; Conservative 44407 44407 44407 44407 44407 44407 44407 44407 4407 23378 32174 32174 32174 32174 16225 133893 31994 31994 Similarity Human LENGTH: 57130 US-09-835-081-3/c ; ORGANISM: Hu US-09-835-081-3 Matches 402; TYPE: DNA Query Match Best Local S 61 000000000000000000000 g ò g ò

AGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGA

239

TCTACTGAAAATAYAAAA--AGCTAGACGTGGTGGCACACCTGTAATCCCAGCTACTT

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GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC

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LENGIH:
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Patent No. US20020132325A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO01158DIV
CURRENT APPLICATION NUMBER: US/10/096,960
CURRENT FILING DATE: 2002-03-14
PRIOR PAPLICATION NUMBER: 09/800,960
PRIOR PRILING DATE: 2001-03-08
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22314 GGGAGGCTGAGGCAGGAGAATTGCTTGAACCCAGGAGGTGGAGGTTGCGGTGAGGTGAGA 22255
                                                                                                   121 GGTGGATCACCTGAA-GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTAT 179
                           TTGCATCATTGCACAATGGAGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCGTC
                                            462 CATGATCCTGCCACTGCACTCCGGCCTGGCCAACAGAGAGGAGCCTGTCTAAAGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%; Score 244.2; DB 12; Length 73.3%; Pred. No. 8.6e-45; ive 3; Mismatches 101; Indels
                                                                                                                                     416 TACTIGGGAGGCAGGGGGTCCACTT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(62804)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                              522 AAAAATAAAGCAACA 536
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Matches 407; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                              US-10-096-960-3
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                                GATIGCATCATTGCACAATGGAGGGGAGCCACCAGCCTGGGCAACAAGAGGAAATCTCCG
                                                                                                                                                   TCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAT-----TAGGCTGGGTGGTGCTGTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 2362, Application US/09880107
; Patent No. US20020112981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Wockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TILLE DF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
; TILLE OF INVENTION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR PRILING DATE: 2000-10-02
; SOFTWARE: Patentin Ver: 2.1
; TENCIN OF 2362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 MS8600 US-09-880-107-2362
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ORGANISM: Homo sapiens
                                      US-09-880-107-2362/c
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11431 CTACTCAGCTGGATTGAGGTGGGAGGATCCCTTGAGCCCAGGAGGTAGAGGCTGCAGTGA 11372
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                                                                                                                                                                                                    Sequence 2209, Application US/09764869
Sequence 2209, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT PILING DATE: 2001-01-17
FILE OF INVENTION OF 1 Femored - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 238.8; DB 10; Length
Pred. No. 1.1e-43;
3; Mismatches 110; Indels
                                                                                                                            11311 AAAAAAAAAAAAA 11295
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Best Local Similarity 72.9%;
Matches 398; Conservative
                                                                                              520 AAAAAATAAAGCAACA 536
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Best Local Similarity
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US-09-764-869-2209
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US-09-764-869-2209
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibo FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file v NUMBER OF SQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 240.2; DB 10;
Pred. No. 4.8e-44;
3; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                       Sequence 1157, Application US/09764847
Patent No. US20020132767A1
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Best Local Similarity 72.7%;
Matches 405; Conservative
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US-09-764-847-1157
           4934 GATCGCACCATTGCA
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US-09-764-847-1157/c
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GENERAL INFORMATION:

APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Cancer Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-09-25
--- GTCCACTTGATGTCGAGACTGCAGTGAGCCATGA 466
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Pred. No. 2.3e-43;
3; Mismatches 135; Indels
                                                                                                                                                               Sequence 292, Application US/09962436 Patent No. US20020081301A1
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OTHER INFORMATION: n=a,t,g or c
                                                                      39550 AAAAAAAAAAAAGGCAG 39566
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                                    527 TAAAGCAACATATCCTG 543
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Matches 388; Conservative
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LENGTH: 65608
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US-09-962-436-292
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                                                                                                                               TITLE OF INVENTION: Decess for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Gene Sets
FILE REPERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/60/234,034
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR PLING DATE: 2000-09-20
PRIOR PLING DATE: 2000-09-20
PRIOR PLING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn Version 3.0
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14.2%; Score 237.8; DB 9;
Best Local Similarity 69.7%; Pred. No. 2.3e-43;
Matches 388; Conservative 3; Mismatches 135;
                                                                  Sequence 180, Application US/09954531 Patent No. US20020165180A1
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): LCCATION: (1)...(65608)

): OTHER INFORMATION: n=a,t,g or c

0S-09-954-531-180
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ORGANISM: Homo sapiens
                                                                                                 GENERAL INFORMATION: APPLICANT: Weaver,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                     APPLICANT: Rosen et al.
TITLE DE INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEO ID NOS-4031
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 237.6;
Pred. No. 1.2
                                                                                               ; Sequence 2903, Application US/09764877; Patent No. US20020147140A1; GENERAL INFORMATION:
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; Sequence 36, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   14.18;
71.68;
    39550 AAAAAAAAAAAGGCAG 39566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          US-09-764-877-2903
                                                                                                                                                                                                                                                                                                               SEQ ID NO 2903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398;
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: |
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                    GENERAL INCOMENTATION:
APPLICANT: Edner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/09/285,077
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 TACTGAAAATAYAAAA--AGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAG
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Pred. No. 2.3e-43;
3; Mismatches 135;
                                                                                                                                     Sequence 119, Application US/09962832 Patent No. US20020110821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: n-a,t,g or
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69.78;
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527 TAAAGCAACATATCCTG 543
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Best Local Similarity 69.7
Matches 388; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 119
LENGTH: 65608
                                                                                                                 09-962-832-119
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Sequence 3, Application US/10003295
Sequence 3, Application US/10003295
Patent No. US20020168741A1
GENERAL INFORMATION:
APPLICANT: GRAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/10/003,295
CURRENT APPLICATION NUMBER: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13833 GGACCGGGTGGCTCACACACACAGTAATCCCAGTACTTTGGGAGGCCGAGGCAGGTG 13774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13487 ACTAGGGAGGCTGAGGCACGAGAATCACTTGAATCTGGGAGGTGGAGGCTGCAGTGAGCC 13428
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Pred. No. 3.2e-42;
2; Mismatches 89; Indels
         PRIOR APPLICATION NUMBER: 60/160626
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/692414
PRIOR APPLICATION NUMBER: 09/692414
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/804076
PRIOR APPLICATION NUMBER: 09/804076
PRIOR APPLICATION NUMBER: 2091-04-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASSESED for Windows Version 4.0
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73.9%;
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatul TITLE OF INVENTION: Sets FILE REPERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn version 3.0
SEQ ID NO 36
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Patent No. US20020123095A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Estrogen receptor alpha variants and
TITLE OF INVENTION: methods of detection thereof
TITLE OF INVENTION: Methods of Getection thereof
CURRENT APPLICATION NUMBER: US/09/933,267A
CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                              Score 235.6; DB 10;
Pred. No. 7.6e-43;
3; Mismatches 112;
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Best Local Similarity 72.0%;
Matches 402; Conservative
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US-09-962-436-36
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US-09-933-267A-1/C
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Length 465237; 37;

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LENGTH: 110096
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LENGTH: 5386
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                             PYPE: DNA
                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11765 GAGTTCAAGATCAGCTTGGACAACACAGTGAAACTCCCATCTGTACAAAAATACAAAAT 11824
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                                                                                                                                                                                                                                                                               1 GAATICAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACAAAATT 60
                                                                                                                                                                                                                                        Gaps
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Fatent No. USZ0020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
FRIOR PEPTICATION NUMBER: US 60/211,379
FRIOR APPLICATION NUMBER: US 60/211,379
FRIOR FILING DATE: 2000-16-14
FRIOR FILING DATE: 2000-66-14
FRIOR FILING DATE: 2000-16-14
FRIOR FILING DATE: 2000-16-14
FRIOR FILING DATE: 2000-16-14
SPRIOR FILING DATE: 2000-16-14
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                   Query Match 13.9%; Score 232.8; DB 9; Best Local Similarity 69.0%; Pred. No. 1.9e-42; Matches 381; Conservative 3; Mismatches 145;
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                               ; ORGANISM: Homo sapiens
US-10-003-295-3
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                                          ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AD000092
US-09-880-107-1542
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Patent No. US20020132753A1
GENERAL INFORMATION:
TTYLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/101-17
PATOR APPLICATION 000 TENDED TO 1792
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 2.6e-42;
2; Mismatches 101; Indels
                                                                                                         Score 232.4; DB 10; Length
Pred. No. 4.2e-42;
2; Mismatches 133; Indels
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Best Local Similarity 72.27
Matches 354; Conservative
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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Sequence 18428 Application US/09880107

Sequence INCORATION:
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
TILE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TILE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFRENCE: 4421-5028-WO
CURRENT FALICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3428
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US-09-880-107-3428
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ORGANISM: Homo sapiens
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GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATC 180
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M33388 Human Cytoc
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X58467 Human CYP2D
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Risinger, C., Andersson, M.K., Lewander, T. and Oliasson, E. TITLE Detection of cyp2d6 polymorphisms JOURNAL Patent: WO 0218638-A 2 07-MAR-2002; Gemini Genomics PLC (GB) FEATURES 1. 1680 /Organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 413 a 379 c 539 g 342 t 7 others	Query Match 100.0%; Score 1680; DB 6; Length 1680; Best Local Similarity 100.0%; Pred. No. 0; No. 0; Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Indels 0; Gaps 0; QY 1 GAATTCAAGACCAGCTGGACAACTTGGAAGACCSGGTCTCTACAAAAATACAAAATT 60 Db 1 GAATTCAAGACCAGCTGGACAACTTGGAAGAACCAGCATTGGAAGAATAATT 60 QY 61 AGCTGGATTGGGTCGGTGGCTCATGATAATCCCAGCACTTTGGGAGCCTCAGGT 120 Pb 61 AGCTGGGATTGGGTCGGTCATGCTAAATCCCAGCACTTTGGGAGCCTCAGGT 120 C 1	0y 181 TCTACTGAAAATAYAAAAAGCTAGACGTGGCACACACCTGTAATCCCAGCTACTTAG 240 181 TCTACTGAAAATAYAAAAAGCTAGACGTGGCACACACCTGTAATCCCAGCTACTTAG 240 0y 241 GAGCTGAGGCAGAGAATTGCTTGAAGCTGAGGTGAAGGTTGAGTCACTTAG 240 0y 241 GAGCTGAGGCAGAGAATTGCTTGAAGCTAGAGGTGAAGGTTGTAGTCAGCCGAGATT 300 0y 301 GCATCATTGCACAATGGAGGGGAGCCACCAGCTGGGCACAAGAGGAAATCTCCGTCTC 360 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0y 481 TCCGGCCTGGGCAACAGAGCCCTGTCTAAAGAAAAAAAAA	QY 721 CATAGCCCGGCCAGAGCCCAGGAATGTGGGCTGGGGGCCGCTCTGGACAGGACT 780
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Catarrhini; Hominidae; Homo.
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         GTGTATGTGTGAATATTGTCTTTGTGTGGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG
                                                                   GTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATG
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                                 CAAGTGTGAACAAGTGGACAAGTGTCTGGGAGTGGACAAGAGATCTGTGCACCATCAGGT
                                                                                                    ATGCCACTCATCATCAGGAGCTCTAAGGCCCCAGGTAAGTGCCAGTGACAGATAAGGGTG
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                                                                                                                                                                                                                                                                               GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG
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Patent: WO 0218638-A 1 07-MAR-2002;
Gemini Genomics PLC (GB)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1 from Patent W00218638.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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join(1620. .1799,2503. .2674,3225. .3377,3466. .3626,
4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658. .5836)
/genen"CYP2D6"
                                                           .5909)
                                                                                 join(1532. 1799,2503. 2674,3225. 3377,3466. 3626,
4060. 4236,4427. 4568,4776. 4963,5418. 5559,5658. 5909)
/gene="CYP2D6"
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BENEKAKGREDESSFNDENLATVVADLESAGKWTTSTTLAWGLLLMILHPDVORRVQDE
IDDVIGGVRRPEMGDQAHMYTTAVIHEVQRFGDIVPLGVTHWTSRDIEVOGFRIPKG
TTLTTNLSSVLKDENRACLGEPLAR
MELFLFTSLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"

1800. .2020
//gene="CYP2D6"
//note="G00-132-127"
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NLLHVDFQNTPYCFDQLRRRFGDVFSLQLAWTPVVVLNGLAAVREALVTHGEDTADRP
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CAAFANHSGRPFRPNGLLDKAVSNVIASLTCGRRFEYDDPRFLRLLDLAQEGLKEESG
join(1532. 1799,2503. .2674,3225. .3377,3466. .3626,
4060. .4236,4427. .4568,4776. .4963,5418. .5559,5658.
/genew CYP2D6"
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/note="G00-132-127; does not fit consensus"
/number=2
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/db_xref="G1:181304"
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/note="G00-132-127"
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/number=3
3466. 3656
/gene="CYP2D6"
/note="G00-132-127"
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/note="G00-132-127"
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/gene="CYP2D6"
/note="G00-132-127"
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/gene="CYP2D6"
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/gene="CYP2D6"
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/gene="CYP2D6"
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Kimura,S., Umeno,M., Skoda,R.C., Meyer,U.A. and Gonzalez,F.J.
The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and
identification of the polymorphic CYP2D6 gene, a related gene, and
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Loganizama-Homo sapiens"

/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                 1057 TGAAGTGAAGGGACCAGGCCCATGATGATCACAGGAGCTCTAAGGCCCCAGGT
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Best Local Similarity 99.5%;
Matches 1638; Conservative
                                                                                                                                                          /number=8
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                                                                                                                                                                                                                                         /number=9
8267. .830
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5617. .586
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5377. .55
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4031. .4207,4400. .4540,4735. .4922,5377. .5518,5617. .5868)
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/gene="CYP2D7BP"
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1031. .4207,4400. .4540,4735. .4922,5377. .5518,5617. .5795)
/gene-"CYP2D7BP"
                                                                                                                    Heim,M.H.

Direct Submission
Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre Submitted (25-MAR-1991) M.H. Heim, Dept of Pharmacology, Biocentre University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND 2 (bases 1 to 13677)
Heim,M.H. and Meyer,U.A.
Evolution of a highly polymorphic human cytochrome P450 gene cluster: CYP2D6
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13677)
                                        CYP2D7BP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene.
Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                              See X58467, and Am. J. Hum. Genet. 47:994-1001(1990).
Location/Qualifiers
1. 13677
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/gene="CYP2D7BP"
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2504. .2675
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  Human CYP2D7BP pset
X58468
X58468.1 GI:30337
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                                                                                                          Direct Submission
Submitted (25-MAR-1991) M.H. Helm, Dept of Pharmacology, Biocentre
Submitted (25-MAR-1991) M.H. Helm, Dept of Pharmacology, Biocentre
University of Basel, Klingelbergstr 70, 4056 Basel, SWITZERLAND
Lebases 1 to 13278)
Helm, M.H. and Meyer, U.A.
Evolution of a highly polymorphic human cytochrome P450 gene
cluster: CYP2D6
Genomics 14 (1), 49-58 (1992)
9305208
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 13278)
X58467. X58467.1 GI:30336 CYP2D7AP gene; Cytochrome P450 2D6; pseudogene. CYP2D7AP gene; Cytochrome P450; cytochrome P450 2D6; pseudogene. Homo sapiens. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  join(1154. .1424,2125. .2296,2823. .2975,3064. .3225,
3611. .3827,4020. .4161,4356. .4542,4998. .5139,5238.
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Location/Qualifiers
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2125. .22
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                                                                         Gaps
                                                                                                                      867 AGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCTGTGTATGTGTGAATATTGTCTTTGTG
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                                               Length 5503;
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                                               Score 721; DB
Pred. No. 0;
0; Mismatches
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               б
             1851
                                                 42.9%;
99.7%;
/number=9
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Chromosome 22.
                                                           Best Local Similarity 99.7
Matches 871; Conservative
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                                                 Query Match
           BASE COUNT
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13733. 13909,14102. 14243,14438. 14625,15080. 15221,
15320. 15496)
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TATA_signal 1276. 1282

prim_transcript 1304. .650

/note="CYP2D8P mRNA and introns"

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   Location/Qualifiers
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/gene="CYP2D8P"
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Draft entry and computer-readable sequence for [1] kindly submitted
by S.Kimura, 29-MAR-1990.
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Kimura, S., Umeno, M., Skoda, R.C., Meyer, U.A. and Gonzalez, F.J.
The human debrisoquine 4-hydroxylase (CYP2D) locus: sequence and identification of the polymorphic CYP2D6 gene, a related gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         944 GTGTAATCGTGTCCCTGCAAGTGTGAACAAGTGGACAAGTGTCTGGGAGTGGACAAGAGA 1003
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debrisoquine 4-hydroxylase.
Human DNA, clones lambda-2D-A and lambda-2D-B.
                                                                                                                                                                                                                                                                                                                                               h 17.1%; Score 287; DB 9; I Similarity 99.7%; Pred. No. 9.4e-138; 37; Conservative 0; Mismatches 1;
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90072069
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1 3664 c 3968 g 2744 t
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KEYWORDS
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cambridgeshire, CBIO 15A, WR. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 25, 2011 this sequence version replaced $1:30.432.

buring sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: FBME; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was finished as follows unless otherwise noted: all regions were
either double-stranded or sequenced with an alternate chemistry or
covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at least one
plasmid subclone or more than one M13 subclone; and the assombly
was confirmed by the sanger centre Chromosome 22,
constructed by the Sanger Centre Chromosome 22 mapping Group.
Futher information can be found at
http://www.sanger.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/Puros.ac.uk/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr22
RP1-257120 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chor1.org/bacpac/home.htm
                                                                            Submitted (22-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone RP1-257120 The true right end of clone RP1-18601 is at 20171 in this sequence.

Location/Qualifiers
1. 1.14846
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//db_xref="Raxon:9606"
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1952. .19153
/note="consensus"
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/note="MER11C repeat: matches 1. .1057 of consensus"
16086. .16507
/note="Libor repeat: matches 1552. .1964 of consensus"
17055. .17127
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'note="20 copies 2 mer ac 82% conserved"
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1093. .1682
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1097. .1600
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/note="match: GSS: Em:AQ563517"
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/note="match: GSS: Em:AQ140240"
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7162. .7366
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1357, ,7396
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'note-"match: STS: Em:HS324WC5"
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/note="CpG island"
/evidence-not_experimental
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  1 (bases 1 to 114846)
                                                    Direct Submission
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Human DNA sequence from clone RPI-257120 on chromosome
22g13.1-13.2, complete sequence.
ALO21878
ALO21878.2 GI:17065905
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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14102. .14243
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//replace="LIP repeat: matches 2378, .2416 of consensus"
//replace="LIP repeat: matches 2318, .2416 of consensus"
//replace="LIP repeat: matches 2311, .2378 of consensus"
//replace="LIP repeat: matches 2294, .2311 of consensus"
//replace="LIP repeat: matches 1445, .2294 of consensus"
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| ### Anote="HERVI repeat: matches 2098. .4455 of consensus" |
| ### Anote="HERVI repeat: matches 2098. .2163 of consensus" |
| ### Anote="HERVI repeat: matches 2098. .2163 of consensus" |
| ### Anote="HERVI repeat: matches 1561. .2163 of consensus" |
| ### Anote="HERVI repeat: matches 1561. .2163 of consensus" |
| ### Anote="HERVI repeat: matches 9. .1561 of consensus" |
| ### Anote="LIRRIDE repeat: matches 1. .510 of consensus" |
| ### Anote="LIRRIDE repeat: matches 1226. .1378 of consensus" |
| ### Anote="LIRBE repeat: matches -656. .1226 of consensus" |
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complement(join(42379. 42591,42916. .43112))
/note="match: STS: Em:c27508"
complement(join(42491. .42603,42916. .42945))
/note="match: STS: Em:G43129"
/note="match: STS: Em:G43129"
/note="ptrs repeat: matches 40. .93 of consensus 44916. .45564
/note="ptrs repeat: matches 5. .671 of consensus 2000 consensus 20
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/note="match: GSS: Bm:AF046780"
26890, .26995
/note="match: GSS: Bm:AZ083430"
27147, .28076
/note="HERVI repeat: matches 4455. .5
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58051, .59084
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54417. 54450
/note="17 copies 2 mer ca 100%
54578. 55083
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65916. .65961
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note="match: GSS: Em:B14069"
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                                                                      /replace="aaaata"
19896. .19939
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/note="match: GSS: Em:AU042256"

/note="match: GSS: Em:AQ533248"

/note="match: GSS: Em:AQ533248"

/note="match: GSS: Em:AQ618257"

note="match: GSS: Em:AQ618257"

note="match: GSS: Em:AQ618257"

note="LIM5A repeat: matches 5857. .6292 of consensus"

note="LIM5A repeat: matches 703. .787 of consensus"

note="MER21B repeat: matches 703. .787 of consensus"

note="MER21B repeat: matches 76. .540 of consensus"

/note="MER21B repeat: matches 76. .540 of consensus"

note="MER21B repeat: matches 76. .540 of consensus"

/note="MER21B repeat: matches 76. .540 of consensus"

/note="match: GSS: Em:B13983"

note="match: Weak data"

/note="match: Weak data"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTG
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Indels
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/note="32 copies 2 mer aa 67% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 269; DB 9;
Pred. No. 1.4e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(107923, .108378)
/note="match: GSS: Em:AQ572846"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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DEFINITION

RESULT 10 AX195173

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ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

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HOMO Sapiens (human)
19 1996027199-A/8
30-JAN-1996
15-JUL-1994 JP 1994164186
FUNAE YOSHIHIKO, IMAOKA SUSUMU, MAT$UKI YASUSHI, HAYASHI KOJI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C C07K16/18,C12N15/09//C12N1/19,C12N9/02,G01N33/53,G01N33/53; CC strandedness: Double; C topology: Linear;
                                                                                                                                                                                                                               /note="coding region"
673. 1315
/note="extended 3' non-coding region, compared to active
P450II sequence, y00300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Homo sapiens.
Home sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutrleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 1494)
Funae,Y., Imaoka,S., Matsuki,Y., Hayashi,K. and Yabusuki,Y.
ANTIBODY RECOGNIZING CYTOCHROME P450206 ORIGINATED FROM MAN
Patent: JP 1996027199-A 8 30-JAN-1996;
See <Y00300> for active P-450IID sequence. See also <X16865> and <X16866> for other sequences exhibiting P-450IID polymorphism. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 61; DB 6; Length 1494; 100.0%; Pred. No. 1.9e-20;
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.3%; Score 89; DB 9; Length 156
Best Local Similarity 100.0%; Pred. No. 5.8e-35;
Matches 89; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type:/liver/
1. .1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding cytochrome P4502D6. E10647 GI:22027703 B10647.1 GI:22027703 Homo canding cytochrome P4502D6. Homo canding cytochrome P4502D6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, 1494
/organism="Homo saplens"
/db_xrefu"taxon:9606"
1 508 c 447 g 291
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                                                              1, ,1563
/organism~"Homo sapiens"
/db_xrefutaxon:9606"
/chromosomew"22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1652 GATAGTGGCCATCTTCCTGCTGGTGG 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   691 GATAGIGGCCATCTICCTGCTCCTGGTGG 719
                                                                                                                                                                           /tissue_type-"liver"
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                                                                                                                                      /clone="pMP34"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMITOMO CHEM CO LTD
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ACCESSION
VERSION
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E10647
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SOURCE
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                                        FEATURES
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                                                                                                                                    PAT 28-AUG-2001
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Ring,H.Z., Hillman,J.L., Yue,H., Azimzai,Y., Yao,M.G., Gandhi,A.R.,
Buygen,D.B., Tang,Y.T., Lal,P. and Bandman,O.
Drug metabolizing enzymes
Patent: WO 0151638-A 26 19-JUL-2001;
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Direct Submission
Submitted (09-0cr-1989) Miles J. S., Imperial Cancer Research Fund,
Laboratory of Molecular Pharmacology, Hugh Robson Building, George
Square, Edinburgh EHB 9XD, U.K
2 (bases I to 153)
GGough, A.C., Miles, J. S., Spurr, N.K., Moss, J.E., Gaedigk, A.,
Eichelbaum, M. and Wolf, C.R.
Identification of the primary gene defect at the cytochrome P450
CCYP2D locus
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1593)
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1543 CCTGCCTGGTCCTCTGTGCCTGGTGGGGGTGCCAGGTGTGTCCAGAGGAGCCCAT 1602
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                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 138; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X16867.1 GI:35203
Cytcchrome; cytochrome P450; polymorphism.
Homo saplens.
Homo saplens
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520 c 470 g 318 t
                                                                                                                                    DNA
                                                                                                                              AX195173 1593 bp
Sequence 26 from Patent WO0151638.
AX195173 4X195173.1 GI:15385736
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/db_xref="taxon:9606"
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Mammalla; Eutheria; Primates;
1 (bases 1 to 1563)
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    Location/Qualifiers
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50729 GGTGGATGGCC 50719
1244 GGTGGATGGCC 1254
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REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS MEDLINE PUBMED

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RESULT 11

PAT 29-SEP-1997

linear

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Gaps

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Length 1563;

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PAT 29-SEP-1997
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1494)
Hayashi,K., Sakaki,T., Yabusaki,Y., Komai,K., Kaneko,H. and Nakatsuka,I.
NETHOP FOR EVALDATING SAFETY
Patent: JP 1996056695-A 17 05-MAR-1996;
SUMITOWO CHEM CO LTD
OS Homo sapiens (human)
PN JP 1996056695-A/17
                                                                                                                                                                                                                                   208279, PR
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Hobase; I to 1494)
Hayashi,K., SakaKi,T., Yabusaki,Y., Komai,K., Kaneko,H. and Nakatsuka,I.
Nakatsuka,I.
Patenti: JP 199605695-A 18 05-MAR-1996;
SUMITOMO CHEM CO LTD
ON HOMO Sapiens (human)
PN JP 1996056695-A/18
PD 05-MAR-1996
PP 15-JUL-1994 JP 1994164184
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PN JP 1996056695-A/17
PD 05-MAR-1996
PP 15-JUL-1994 JP 1994164184
PR 20-JUL-1993 JP 93P 201120, 30-JUL-1993 JP 93P 208279
17-JUN-1994 JP 94P 136053
PL TAYASHI KOJI, SARAKI TOSHIYUKI, YABUSAKI YOSHIYASU, PI
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism='Homo sapiens'
1. 1494
/product='human cytochrome P450 2D6'.
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E10869.1 GI:22027963
JP 1996056695-A/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1.1494
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 509 c 446 g 291
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                                                                                                                                                                                                                                                                                       KANEKO HIDEO, NAKATSUKA IWAO
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strandedness: Double;
topology: Linear;
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       E10868.1 GI:22027962
JP 1996056695-A/17.
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                                    Homo sapiens.
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1 (bases 1 to 1944)
Hayashi,K., Saki,T., Yabusaki,Y., Komai,K., Kaneko,H. and Nakatsuka,I.
Parento Fook EvaLuaring Safery
Patent: JP 1996056695-A 16 05-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        208279, PR
                        1620 AIGGGGCIAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTG 1679
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PR 20-JUL-1993 JP 93P 201120, 30-JUL-1993 JP 93P 20827
17-JUN-1994 JP 94P 136053
PI HAYASHI KOJI, SAKAKI TOSHIYUKI, YABUSAKI YOSHIYASU, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product='human cytochrome P450 2D6'.
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1. 1.9e-20;
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cDNA encoding human cytochrome P450.
E10868
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C1201/02,C12M1/34,C1201/26;
strandedness: Double;
tcpology: Linear;
hypothetical: No.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 508 c 446 g 292
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JP 1996056695-A/16
05-MAR-1996
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JP 1996056695-A/16.
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 Conservative
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Homo sapiens
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PAT 01-SEP-2000
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Unclassified.
1 (bases 1 to 1566)
Wolf,C.Roland., Miles,J.Stephen., Spurr,N.Kay. and Gough,A.Charles.
Genetic assay
Patent: US 5981174-A 22 09-NOV-1999;
Location,Qualifiers
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Wolf,C.Roland., Miles,J.Stephen., Spurr,N.Kay. and Gough,A.Charles.Genetic assay
Patent: US 5981174-A 13 09-NOV-1999;
Location/Qualifiers
1. 1566
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tive 0; Mismatches 0; Indels
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                         1. 1494
/organism:"Homo sapiens"
/db_xref:"taxon:9606"
a 507 c 447 g 29
           Location/Qualifiers
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Matches 61; Conservative
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AR084365
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Homo sapiens.
Eukaryota: Matazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1494)

2 (batary 1.

2 (batary 1.

3 (barryone CER EVALUATING SAFETY

4 (batary 2.)

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         208279, PR
1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTG 1679
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                                                                                                                                                                                                                                   1. .1494
/organism~'Homo sapiens'
1. .1494
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Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 61; Conservative 0; Mismatches 0;
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/db_xref~"taxon:9606"
a 508 c 447 g 291
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AUTHORS
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SOURCE
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TDTTITILSSVLKDEAAVGCHPPEHFLDAQGHFVRPEAFLPFSAGRRACLGEPLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and printed copy of sequence for [1] kindly provided by D.W.Nebert, 15-JUL-1988.
Location/Qualifiers
                                                                                                                                                                                                                                  PRI 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1567)
Gonzalaz, F.J., Vilbols, F., Hardwick, J.P., McBride, O.W.,
Nebert, D.W., Gelboin, H.V. and Meyer, U.A.
Numan debrisoquine 4 Hydroxylase (P450IID1): cDNA and deduced amin acid sequence and assignment of the CYP2D locus to chromosome 22
                         ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTG 1679
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                                          MELFLFFTSLLQHFSFSVPTGQPRPSHHGVFAFLVSPSPYELCAVPR"
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Pred. No. 1.9e-20;
Mismatches 0; Indels
                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                    1567 bp mRNA lin
Human cytochrome P450 dbl mRNA, complete cds.
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cytochrome P450; debrisoguine 4-hydroxylase.
Human hepatocyte, cbnA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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KEYWORDS
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MELFLFFFSLLQHFSFSVPTGQPRPSHHGVFALVSPSPYELCAVPR"

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Submitted (30-JUN-1988) Nebert D.W., NIH, Bethesda, Maryland 20892
see also X07618 (variant a), X07619 (variant b) and X07620 (variant
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Socialez F.J., Skoda,R.C., Kimura,S., Umeno,M., Zanger,U.M.,
Nebert,D.W., Gelboin,H.V., Hardwick,J.P. and Meyer,U.A.
Characterization of the common genetic defect in humans deficient in debrisoquine metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTGCTGGTG 1679
                                                          Gaps
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                 Score 61; DB 6; Length 1566;
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                                                        Indels
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                                     1.9e-20;
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1.9e-20;
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cytochrome P450; cytochrome P450 db1.
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100.0%; Pred. No. ...
                                   Pred. No. 1.9
Mismatches
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88122614
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1. .1567
3.6%; SCOL.
100.0%; Pre
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527 c 465 g
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1567
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Nebert, D.W.
                                                    Conservative
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Best Local Similarity 100.0
Matches 61, Conservative
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ORIGIN
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AUTHORS
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PAT 01-SEP-2000

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172611 bp DNA 11near PRI 09-JAN-2002 AC019129 GI:16077059 HTG.
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Wolf.C.Roland., Miles,J.Stephen., Spurr,N.Kay. and Gough,A.Charles.
Genetic assay
Patent: US 5981174-A 21 09-NOV-1999;
Location/Qualiflers
1. 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 17261.) Sulston, J.E. and Waterston, R.
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Trani,L., Abbott,A. and Creason,K.
The sequence of Homo sapiens BAC clone RP11-559M23
Unpublished (2001)
3 (bases 1 to 172611)
Waterston,R.H.
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Pred. No. 1.9e-20;
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                                                                                                     DNA
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Sequence 21 from patent US 5981174.
AR084373.
AR084373.1 GI:10011144
                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
529 c 468 g
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4 (bases 1 to 172611)
Waterston, R. H.
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5 (bases 1 to 172611)
Waterston, R.
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Matches 61; Conservative
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Unclassified.
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Homo sapiens
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1. .1494
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TTLITNLGSVLKADAVWERPFRFPEHFLDAQGHFVWFPEAFLERAVRR
TTLITNLGSVLKADAVWERPFRFPEHFLDAQGHFVWFPEAFLPFSAGRRACLGEPLAR
MELFLFFTSLLQHFSFSVPTGQPRRPSHHGVFAFLVSPSPYELCAVPR"

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Wolf,C.Roland., Miles,J.Stephen., Spurr,N.Kay. and Gough,A.Charles. Genetic assay
Patent: US 5981174-A 20 09-NOV-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.9e-20;
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14518. .14566
/rpt_family="T-rich"
15603. .15624
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5162. .5399
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059. .7098
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4953. .4976
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6755, .7031
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(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The clone sequenced to the left is ACO87053; the clone sequenced to the right is RPI1-24I5, 2000 bp overlap. Actual start of this clone is at base position of RPI1-559M23; actual end is at base position 10f RPI1-24I5.
                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male
Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, on Oct 12, 2001 this sequence version replaced gi:15624993.

Center: Washington University Genome Sequencing Center
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230. .3551
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3209. .3259
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977. .2082
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739. .1964
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3406. .3426
                                                                                                           Center code: WUGSC
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Sequence Validation:
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                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Homo sapiens
Bukaryota, Springle Craniata; Vertebrata; Euteleos Bukaryota; Butheria; Eutheria; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155401)
Iadonato, S. P., Yu, J., Wong, G.K.-S., Magness, C.L., Green, E.D. Green, P. and Olson, M.V.

Large-scale MCD Mapping and Sequencing of Human Chromosome 7 Unpublished
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Bubb.K.L. and Desmarais,C.L.
Direct Submission
Submitted (13-MAY-1999) Human Genome Center, University Washington, Box 352145, Seattle, WA 98195, USA
OVERLAPPING Sequences:
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                                                                                                                                                                                                                                                                                                                                   Length 172611;
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                                                                                                                                                                                                                                                                                                                      DB 9; Leus
1, 8.4e-21;
0;
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                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                 3.6%; Score 61;
100.0%; Pred. No.
                                                                                            17238. .17264
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17347. .17732
                                                                                                                                                                                                                                                                   /rpt_family="(TTTG)n"
19412. .19455
                                                                                                                                                                 1/76/. .1/854
/rpt_family="MER53"
18006. .18289
/rpt_family="MaLR"
18361. .18553
                                                                                                                                                                                                           /rpt_family="Alu"
17238. 17255
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16681. .16978
/rpt_family="Alu"
16979. .17051
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                                                                                                                                  /rpt_family="L2"
17767. 17864
                                              /rpt_family="L2"
17123. .17255
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Best Local Similarity
Matches 61; Conserv
   repeat_region
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AC007551/c
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This sequence has been validated by Multiple Complete Digust. fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600) are not resolved in the fingerprint and honce do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines. 5951.00 8250.00 1930.00 7724.00 786.00 4548.00 3017.00 652.00 7510.00 6339.00 18377.00 18231.00 7642.00 16345.00 5573.00 2920.00 638.00 3665.00 714.00 3143.00 957.00 813.00 1013.00 2109.00 2151.00 1330.00 958.00 9674.00 3366.00 1519.00 9211.00 NSII 9348.00 2239.00 2128.00 1342.00 3037.00 7685.00 7685.00 7685.00 4577.00 3173.00 982.00 9745.00 2128.00 3425.00 1500.00 669.00 6318.00 5903.00 8292.00 1967.00 16295.00 5590.00 2922.00 669.00 3630.00 810.00 716.00 969.00 810.00 982.00 FЪ 1471.00 4501.00 1721.00 5016.00 1544.00 1518.00 2814.00 9070.00 6603.00 5192.00 585.00 750.00 1122.00 1150.00 7714.00 7740.00 10502.00 10436.00 2254.00 2303.00 8252.00 2682.00 1024.00 9647.00 531.00 17406.00 17191.00 1414.00 615.00 3068.00 1111.00 2361.00 7592.00 1992.00 10621.00 6378.00 6313.00 ECORI 1494.00 4522.00 1714.00 8383.00 2668.00 1038.00 769.00 5002.00 1122.00 9711.00 1554.00 3074.00 2419.00 532.00 558.00 1494.00 2783.00 6602.00 10775.00 1432.00 614.00 7714.00 9024.00 5181.00 1987.00 FЪ 3753.00 2650.00 2667.00 4794.00 4702.00 00.6669 00.0889 3411.00 3350.00 1258.00 1279.00 6992.00 5823.00 4581.00 5623.00 10546.00 10571.00 5285.00 1632.00 1618.00 929.00 1169.00 1162.00 6187.00 1353.00 4273.00 4302.00 1012.00 3687.00 3703.00 4288.00 1457.00 1091.00 3800.00 7354.00 6484.00 6657.00 1146.00 3380.00 5089.00 Sed ---Bglii

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Submitted (09-JAN-2002) Department of Genetics, Washington
Submitted (09-JAN-2002) Department of Genetics, Massouri 63108, USA
Onlyersity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Onlyersity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Onlyersity, 4444 Forest Park Avenue, Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 200807)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                              Db 69498 TAATCCCAGCACTTTGGGAGCCTGAGGTGGGTGGATCACCTGAAGTCAGGAGTTCAAGAC 69439
                                                                                                                                                                                                                                                                                                                                                           92 TAATCCCAGCACTITGGGAGCCTGAGGTGGGTCACCTGAAGTCAGGAGTTCAAGAC 151
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC073278 200807 bp DNA linear PRI 09-J
Homo sapiens BAC clone RP11-661L8 from 7, complete sequence.
AC073278
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                 Length 155401;
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Harris,A., Abbott,A., Boyer,E. and Elliott,G.
The sequence of Homo sapiens BAC clone RP11-661L8
10 (bases 1 to 200807)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 9; I
Pred. No. 2.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                   3.6%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                             /rpt_family="Alu"
complement(38886. .44355)
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30875. 31174
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36417. .36660
                                                                                                                                                                                           /rpt_family="Alu"
38028. .38321
                                                                                                                             /rpt_family="L1"
36878. .37160
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                                                                                                                                                                                                             .38321
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Waterston, R.H.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                  Unmatched fragments are due to vector-containing sequences. We expect 3, 1 and 1-2 such fragments in the BqIII, EcoRI, and NsiI enzyme domains. respectively. The sum of these fragments can be calculated from the sequence of the BAC clone and, in this clone, should be 9458, 8782, and 13404 for the three enzyme domains.
                                                                                           2421.00
                                                             516.00
                                       2447.00
           3340.00
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13475.00
           3281.00
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complement(22738. .22868)
/rpt_family="MLT1"
complement(22728. .22868)
23222. .23481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2641. .2920)
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complement(4878. .5175)
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complement(6199. .6487)
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complement(20444. .20581)
/rpt_family="Alu"
complement(22334. .22414)
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complement(7895. .8179)
/rpt_family="Alu"
8298. .8602
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24318. .24857
/rpt_family="LTR1"
complement(25363. .25680)
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/chromosome="7"
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/rpt_family="Alu"
9907 . .10185
/rpt_family="Alu"
11405 . .11901
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12136, 19900
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23871. "
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                              4784.00
        1819.00
                                                                                          12034.00 11986.00
                                                                                                                                    4794.00 4752.00
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/rpt_family~"(CA)n"

'rpt_family-"L1"

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'rpt_family-"Alu"

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/rpt_family-"L2"
11502 .11745
/rpt_family-"Alu"
11577 .11600
/rpt_family-"AT_rich"
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7986. .8010
/rpt_familyo"AT_rich"
8031. .8053
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8054. .8418
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6430. .6684
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6826. .6932
/rpt_familyu"(TA)n"
6932. .7226
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9175. 9452
/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa.K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                          The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-627E12; the clone sequenced
to the right is RP5-1102A12, 2000 bp overlap. Actual start of this
clone is at base position 1 of RP11-661L8.
                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were dobble stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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    .200807
    /organism="Homo sapiens"
/db_xrefn"taxon:9606"
    /chromosome="7"

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3357. 3458
/rpt_family="C-rich"
3456. 3503
/rpt_family="(TTTTC)n"
3480. 3784
/rpt_family="Alu"
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2615. .2768
/rpt_family="CT-rich"
2752. .3035
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/clone="RP11-661L8"
/clone_lib="RPCI-11"
38. .98
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1. .200807
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17th family Alu"

1113. 1410

/rpt_family Alu"

/rpt_family Alu"

2202. 2308
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/rpt_family="Alu"
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7574. .7599
7574. .7599

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/rpt_family."A-rich" 10412. .10476 rpt_family "T-rich" 0451. .10753

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.11501

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rpt_family~"Alu" 900. 9936

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Submitted (26-JUN-2002) Department of Genetics, Washington
Submitted (26-JUN-2002) Department of Genetics, Missouri 63108, USA
Only 24, 2001 this sequence version replaced gi:8468974.
Genome Center
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Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (Dases 1 to 190349)
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4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 190349) Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                  Db 131148 CGTGGTGGCACACACCTGTAATCCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTT 131206
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                               206 CGTGGTGGCACACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTT 264
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens BAC clone RP11-285F23 from 2, complete sequence. AC009475 GI:15004913
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Waterston, R. H.
Direct Submission
Submitted (24.AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
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The sequence of Homo sapiens BAC clone RP11-285F23
Unpublished (2001)
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                               Score 59; DB 9; L
Pred. No. 8.9e-20;
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Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (12-JUN-2000) Genome
University School of Medicine,
/rpt_family="AT_rich"
12550. .12690
                                                                /rpt_family="L1"
13141. 13440
/rpt_family="Alu"
13441. 13692
                           /rpt_family="Alu"
13003. .13140
                                                                                                                                        /rpt_family="L1"
13693. .13978
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Waterston, R.H.
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Waterston, R.
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Matches 59; Conservative
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AC009475/c
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                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
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TITLE
JOURNAL
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PUBMED
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                               NOOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACC3.6
                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone, and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-285F23; actual end is at base position 190349 of RP11-285F23.
Location/Qualifiers
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1657. .1950
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                          Center project name: H_NH0285F23
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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92. .356
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3144. 3191
/rpt_family="(GA)n"
3506. 3555
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2198. .2256
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3118. .3144
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/map="2"
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repeat_region

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Direct Submission

Submitted (20-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Lambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jul 24, 2002 this sequence version replaced gi:18564638.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone: and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl RP3-476K8 is from the library RPCI-3 constructed by the group of bieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Human DNA sequence from clone RP3-476K8 on chromosome 1, complete
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107415)
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                                                                                      Length 190349;
                                                                                3.5%; Score 30; 100.0%; Pred. No. 3e-19; 1100.0%; Pred. No. 3e-19; 11ve 0; Mismatches 0; Indels
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/clone_lib="RPCI-3"
29399 a 25329 c 25209 g 27478 t
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/organisme"Homo sapiens"
/db_xrefe"taxon:9606"
                            /rpt_family~"(CAAAA)n"
33607. .33687
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      33586. .33605
                                                                                                          Best Local Similarity 100.
Matches 58; Conservative
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                                                                                         Query Match
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AL513365/c
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/rpt_family~MIR"
17187. 17591
/note-"match to EST BG900533 (NID:914310782)"
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77026. .27525
'rpt_family="MaLR"
7750. .28230. .28230.
7750. .27936
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/note-"match to EST BG563093 (NID:gl3570745)"
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/rpt_family-"MER1_type"
33304. .33606
/rpt_family-"Alu"
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2961. .32995
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22158, .22381
/rpt_family="MaLR"
22382, .22933
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                                                                                                                                                                                                                                                                                                                  7442. .18212
note="match to EST
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3954. .23992
rpt_family="(TG)n"
                                                                                                        /rpt_family~"ERV1"
14821. 1600
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20448. 20748
/rpt_family-"Alu"
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6007. 16107
                                                                                    /rpt_family~"ERVl"
14666. .14763
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/rpt_family-"L2"
28982. .29264
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'rpt_family="Alu"
1829. .z1869
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2615. 3201.
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/rpt_family~"Alu"
13007. .13990
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/rpt_family="L1"
26139. .26351
                                13007. .13990
/rpt_family."Ll"
14340. .14665
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Pred. No. 3.3e-18;

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Best Local Similarity 100.
Matches 56; Conservative
                                                                                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bird,C.
Direct Submission
Submitted (09-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (09-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 15, 2002 this sequence version replaced gi:17138620.
Draft Sequence Produced by Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                      Au. 3443 173519 bp DNA linear HTG 13-AUG-2002 PROGRESS ***, in ordered pieces. AL732423 AC017058 AL732423 II GI:22265447
                                                              .:
0
                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAPH; version 4.5
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-primer-amersham; 24% of reads
Chemistry: Dye-terminator; 69% of reads
Chemistry: Dye-terminator; 69% of reads
Chemistry: Dye-terminator Big Dye; 5% of reads
Consensus quality: 173499 bases at least 040
Consensus quality: 173519 bases at least 020
Consensus quality: 173519 bases at least 020
Insert size: 173519; sum-of-contigs
Insert size: 176928; 4.2% error; agarose-fp
Quality coverage: 11.02x in 020 bases; sum-of-contigs Quality
coverage: 10.88x in 020 bases; agarose-fp
                                                              Gaps
                                                                                                                Db 67252 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCC 67197
                                                                                          121 GGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCC 176
                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 173519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by the finished sequence as soon as it is available and the accession number will be preserved.
                                                            0;
                   Length 107415;
DB 9; Leus
7, 3.6e-18;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:03759
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37820 c 37404 g 45761 t
                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Summary Statistics
                 Score 56;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
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3.3%; Sco.
100.0%; Pre
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          Query Match 3.3
Best Local Similarity 100.
Matches 56; Conservative
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AL732423/c
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Length 173519;

DB 2;

3.3%; Score 56;

Query Match

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NEANDYD.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, C., Burch, D., Burkett, C., Burch, B., Burkett, M., Biown, B., Bryant, N.P., Burbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Burkett, C., Burch, M., Bryant, N.P., Charcon, T., Carron, T.F., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Carron, T.F., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D., Davila, M.L., Davy, Carroll, L., Dadgarich, D.A., Davila, R., Davila, R., Davila, M.L., Davy, Carroll, L., Dadgarich, D.A., Davila, M.L., Davy, Carroll, L., Dang, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Bannart, C., Edgar, D., Edwards, C.C., Elhaj, C., Becotto, M., Ealls, T., Ferraguco, D., Flagg, N., Footer, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Guner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Guner, T., Garza, N., Gill, R., Gabisi, J. H., Guevara, W., Gunaratne, P., Hawes, A., Hen, X., Harris, C., Harris, K., Hang, M., Hulyks, S., Karlsson, E., Karlsson, E., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louser, K., Martina, R., Martina, E., Martin, R., Martina, E., Martin, R., Martina, M., Manches, M., Mei, G., Metzker, M., Mencris, S., Mattin, R., Martin, R., Morter, M., Melson, D., Newtson, M., Noorish, T., Morter, M., Ren, Y., Rives, M., Norison, M., Polak, M., Panes, M., Panes, M., Panes, M., Panes, M., Panes, M., Panes, M., Tanes, J., Tanestis, A., Tanestis, R., Wall, Martinger, R., Wallalon, D., Villalon, D., Vinson, S., Williamson, A., Waller, R., Waller, R., Waller, R., Waller, R., Waller, R., W
                                                                                                                                                                                                                                                                                                                                                                                           AC080014 163111 bp DNA linear PRI 16-MAY-2002
Homo sapiens 3q BAC RP11-301G23 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     Gaps
                                                                                                                                                                      Db 32966 GGGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACC 32911
                                                                                                                                   120 GGGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACC 175
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0
                                                                     Indels
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0
                                                                 Mismatches
100.08; Pit
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Unpublished
2 (bases 1 to 163111)
Worley, K.C.
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Direct Submission
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TITLE
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AUTHORS TITLE

JOURNAL

COMMENT

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Length 163111;
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Pred. No. 1.1e-17;
0; Mismatches 0;
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/rpt_family~"MIR"
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                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="LIPA7"
complement(16016. 16132)
/rpt_family="FLAM_C"
17586. 17724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(25826, .25871)
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complement(25872, .26178)
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                                                                                                          complement (9671. .10122)
                                                            complement(9534. 9670)
/rpt_family="MIR"
complement(9671. 10122)
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23721. 23816
/rpt_family="(CCCA)n"
24296. 24443
    /rpt_family="AT_rich"
8826. .8856
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name.."6896"
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                                                                                                                                                                                                                                                                                                                                /rpt_family="Alux"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="(A)n"
9317. .19411
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[3961. .15866
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:0418. .20620
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Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                             CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the Insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                          Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 1, 2002 this sequence version replaced gi:18449677.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
Submitted (01-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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/chromosome="3"
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complement(7727. .7943)
/rpt_family."MIR"
8764. .8795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3663, 3842)
/rpt_family~"MER5A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family "(TATATG)n"
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6940. .7252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="RP11-301G23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .163111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121. .431
/rpt_family~"Alux"
1709. .1765
/rpt_family~"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_family "L1ME2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5831
                                                                                                                                                                                                                                                                                                                                                                                                                                    ANNOTATION OF FEATURES:
                                                                (bases 1 to 163111)
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                                                                                    Worley, K.C.
Direct Submission
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source

FEATURES

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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submist. A. and Zody, M.

Direct Submission
Submitted (19-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 19, 2002 this sequence version replaced gi:21699439.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997) http://fp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-5316"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                    Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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complement(7148. 7327)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                   Center project Information
Center project name: L2559
Center clone name: 53_1_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
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/rpt_family="MER33"
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/rpt_family="AluJb"
complement (5704. .6004)
/rpt_family="AluSc"
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9512. .9547
/rpt_family="L2"
complement(9548., .9686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2973)
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/rpt_family="LIMC/D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .7105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="CT-rich" complement(304. .597) /rpt_family="Aluyas" 1544. .1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="AluSp/q"
510. .3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AluSg/x"
4984. .5284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'rpt_family="(TAGA)n"
513. .6797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3946. .4250
/rpt_family="AluSx"
/686. .4912
                                                                                                                                                                                                                                                               Genome Center
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798. .7121
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complement(2664. .2)
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complement(7052. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="18"
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                                                             TITLE
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Burren, Burnisason

Burren, Burnisason

CE Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 17622)

Burren, M. Bastien, V. Bonder, E. Ali, A., Allen, N., Anderson, S., Barren, M. Bastien, V. Charg, J., Chang, J., Mathew, R., Lindblad-Toh, K., Liu, G., Maclarth, M., Meldrim, J., Meneus, L., Mihova, T., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Minon, T., Mathews, C., McCarthy, M., Perre, M., Raymond, C., Retta, R., Rise, C., Rogov, P., Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Perreron, T., Spencer, B., Schauer, S., Schubback, R., Seanan, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schubback, R., Seanan, S., Severy, P., Smith, C., Spencer, B., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Chang, C., Change, T., Ender, E., All, A., Allen, N., Anderson, S., Barna, M., Bassielen, V., Boyalaavak, L., Cooke, M., Barna, M., Bassielen, V., Boyalaavak, L., Chang, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Rarceira, P., Chang, J., Mathew, C., Karatas, A., Kells, C., Lander, E., All, A., Allen, R., Lander, B., Cand, J., Mathew, Matheria, P., Dearellano, K., Dewar, K., Linde, M., Mells, C., Lander, E., Lander, R., Mathe, M., Bassielen, V., Rodne, J., Motard, M., Mells, C., Lander, P., Dearelland, M., Goge, D., Galagan, J., Motard, J., Mathew, S., Schauer, S., Schauer, S., Schauer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signation, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Browh, A., Castle, A., Collans, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galdgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McCurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, P., Peterson, K., Pollara, V., Kiley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wwman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                     PRI 19-JUL-2002
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         Homo sapiens chromosome 18, clone RP11-5316, complete sequence.
AC011825
                                                                                     linear
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 176222)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-5316
                                                                                     DNA
                                                                                  176222 bp
                                                                                                                                                              AC011825.13 GI:21909530
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 176222)
                                                                                                                                                                                                                               Homo sapiens.
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                    RESULT 31
AC011825/c
LOCUS
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TITLE
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REFERENCE
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel costomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dases 1 to 17884)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,

Brottler,P., Cattolico,L., Barbe,V., Pelletier,E., Artigucnave,F.,

Gyapay,G., Saurin,W. and Weissenbach,J.

Unpublished

2 (Dases 1 to 178834)

Genoscope.
                                                                                                                                                                                                              Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dbSTS:STS42873
Identified using the e-PCR software (G. Schuler)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percentage of bases with a quality value > 40 : 97 %.
                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 2.0
Quality coverage: 6.85x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                               Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"R-471B22"
/clone_lib:"RPCI-11"
57571. ,57795
/note-"matching EMBL:RH53500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72275. .72417
/note="matching EMBL:U12022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72576. .72835
/note-"matching EMBL:U12022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72697. .72936
/note="matching EMBL:M78311
RHdb:RH95544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 178834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome~"14"
  AL512791.3 GI:15282123
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Overall quality chart :
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                 HTG; HTGS_ACTIVEFIN
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                                       Comp.c....
/rpt_family."Lima.
19540. 19666
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complement(16847. 17006)
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complement(17007. 17298)
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complement(17007. 17298)
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13678. .13981
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/rpt_family-"L3"
complement(15989. .16289)
/rpt_family-"Alusp"
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                                                                                                                                                                                                                                                                                                             /rpt_family="AluJo"
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complement(16430. 16618)
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20128. .2012
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An Unpublished

Industrian Andan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R.,

Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R.,

Rhicks, P., James, R., Loretz, C., Lasky, S., Madan, A., Ratcliffe, A.,

Shaffer, T. and Hood, L.

Direct Submission

AL Submitted (07-FBB-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 9195, USA

3 (bases I to 185402)

AS Madan, A., Rowen, L., Qin, S., Abbasi, N., Dors, M., Dickhoff, R.,

Harrison, G., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S.,

Ratcliffe, A., Shaffer, T. and Hood, L.

Submitted (21-JUJ-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 9195, USA

On Jul 21, 1999 this sequence version replaced 91:4235135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jóin(23661. .23663,26493. .26523,27687. .27830,30290. .30396,
30807. .30942,31117. .31145)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNP
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AAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTAK"
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Harrison, G., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Statcliffer, A., Shaffer, T. and Hood, L. Sequencing of human chromosome 14 Unpublished
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/note="low quality data"
122750. .123220
/note="low quality data -- this region was resistant to several finishing strategies, especially in the microsatellite"
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        QY
        213 GCACACACCTGTAATCCCAGCTACTTAGGACGCTGAGGCAGGAGATTGCTTGAA
        267

        Db
        55530 GCACACACTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAATTGCTTGAA
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100.0%; Pred. No. 1.1e-17;
ive 0; Mismatches 0;
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46161 a 45067 c 45138 g 49036
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1. .185402
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/protein_id="AAD45181.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="14"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185402)
Madan,A., Rowen,L., Qin,S., Abbasi,N., Dors,M., Dickhoff,R.,
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Homo sapiens chromosome 14 clone BAC257P13 map 14q31, complete
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72824, .72973
                                                                                                                                                  Identified using the e-PCR software (G. Schuler)" 73279. .73383
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74930. .75079
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Identified using the e-PCR software (G.
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Identified using the e-PCR software (G. 75060. .75190
/note="matching EMBL:R26115
                                                                                                                                                                                                                                                  Identified using the e-PCR software 73374. 73474
Anotes"matching EMBL:M86162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identified using the e-PCR software 99189. 93349. //note="matching EMBL:G07510 RHdb:RH96271
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1.1e-17;
                                                /note="matching EMBL:F05082
RHdb:RH100955
RHdb:RH53917
RHdb:RH14408
                                                                                                                                                                           /3279. .73383
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                                                                                                                                                                                                                                                                                                                                                                                          /note="matching EMBL: Z38389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /4933. ./>vos4
/note="matching EMBL:Z38389
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40904 c 41487 g 49203 t
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100.0%; Pred. No. 1.1
:ive 0; Mismatches
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AC006536.2 GI:5542034
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferrelra, P., Fitzhugh, W., Eorrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Joneso, C., Kann, L., Kardles, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Merdrim, J., Maclork, A., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, Wu, J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, Wu, J., Zimmer, A. and Zody, M.
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran N., Bastlen, V., Bloom, T., Dewar, K., Diaz, J. S., Dodge, S., Gandarda, J., Chang, J., Chargaro, B., Chopell, Y., Collymore, A., Cooke, P., Dekardlano, K., Dewar, K., Diaz, J. S., Dodge, S., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illey, I., Johnson, R., Jones, C., Ramat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Ludic, MacLean, C., MacGonald, P., March, T., Mathory, T., Margos, B., Marcarthy, M., Relafinh, J., Mendeus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Naylor, C., Norman, C. H., O'Connor, T., O'Connor, T., O'Donnell, P., O'Neil, D., O'Liver, J., Peterson, K., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., Machar, M., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retrack, S., Sepery, P., Shinkhang, P., Pierre, N., Raymond, C., Retrack, S., Sepery, P., Shinkhang, P., Pierre, N., Raymond, C., Retrack, S., Sepery, P., Shinkhang, P., Pierre, N., Wann, N., Stojanovic, N., Talama, J., Zenbek, L., Zimmer, A. and Zody, M.

Direct submission

M. Submitted (G. Jull, 2002) Whitehead Institute/MIT center for Genome Research, 330 Charles Street, Candary, L., Boukhgatter, B., Gook, P., Clang, J., Chang, J., March, J., Matthows, C., Kartas, A., Karts, A., Hagos, E., Karts, A., Hagos, S., Gerter, A., McChonc, T., Halle, W., Gae, D., Galagan, J., McChon, C., Norman, C., Norman, C., Norman, J., Halle, W., Seplanor, B., Schanger, D., Dodge, S., Grander, M., Schauer, S., Schupback, M., Schauer, S.
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                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           1 (bases 1 to 214984)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-344B2
                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 214984)
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                                                                   Homo sapiens
                              SOURCE
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
Conter project name: Li004
Center project name: 344_B_2
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complement(683. .970)
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/rpt_family="Charliel"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'rpt_family="FLAM_C"
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                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            /clone="RP11-344B2"
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                                                                                    Center code: WIBR
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Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Eckenberg, R., Brulls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14
                                                                                                                                         Direct Submission
Submitted (01-AUG-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                  dbsrs:srs65858
Identified using the e-PCR software (G. Schuler)"
217007. 217161
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/note="matching EMBL:M78553
                                                                                                                                                                                            - Web : www genoscope.cns.fr)
On Jul 8, 2001 this sequence version replaced gi:14271969.
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/note="matching EMBL:AA431184
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Contact: SeqRef@genoscope.cns.fr
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44482. 44349
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Range : bases
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Bummalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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complement(15099..15237)
/rpt_family="MERSB"
complement(15318..15405)
/rpt_family="L1MB4"
                                                                 /rpt_family="Alu"
complement(6183. .6491)
/rpt_family="Alur"
6800. .771
                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alusq"
11292. .12391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(13251. .13510)
/rpt_family="AluJb"
13512. .13602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(12884. .13148)
/rpt_family="AluJo"
13155. .13250
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complement(14888. 15002)
                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alusx"
complement(10260, .1060?\/rpt_family="Alusx"
                                                                                                                                                                                                                                           complement 8215. .8480)
/rpt_family="L3"
complement (8516. .8846)
/rpt_family="L3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55;
Pred. No.
   complement(5633. .6104)
/rpt_family="MER41B"
                                    51077. .6128
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="CT-rich"
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13616. .13795
/rpt_family="MER5A"
14787. .14809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="LTR16C"
2725. .12881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "LTR16C"
                                                                                                                                                                                       /rpt_family="LTR30"
7857. .8074
/rpt_family="pTR5"
                                                                                                                                                                                                                                                                                                                                  /rpt_family="AluJb"
9579. .9884
                                                                                                                                                                                                                                                                                                                                                                     'rpt_family="AluJb"
                                                                                                                                                  )800. .//JL
/rpt_family="pTR5"
/756. .7853
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12588. .12687
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Best Local Similarity
Matches 55; Conserv
     repeat_region
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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                          This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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/note="single stranded/single chemistry region"
66729. .66731
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/clone:"CTB-415D8, SCb-332a23"
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/organism∵"Homo sapiens"
/db_xrefo"taxon:9606"
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/db_xref="taxon:9606"
/clone="SCb-332a23"
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/clone:"CTB-415D8"
96358. .265308
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                                                                                                                                                Sequence Quality Assessment:
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Reichwald.K. and Platzer.M.

Direct Submission

L. Submitted (23-AUG-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany Gasadiqui.R. and Platzer.M.

Direct Submission

L. Submitted (05-ARP-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 4 (bases 1 to 265308)

Helmack.L. and Platzer.M.

Direct Submission

L. Submitted (28-JUN-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Butchnology, Beutenbergstrasse 11, Jena 07745, Germany Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Chases 1 to 265308)

L. Submitted (28-JUN-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Chases 1 to 265308)

L. Lagemann, D. and Platzer, M.

Direct Submission

E. Lagemann, D. and Platzer, M.

Direct Submission

E. Lagemann, D. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (thase 1 to 265308)
Schudy, A., Schlibabel, M., Baumgart, C., Menzel, U., Weber, J., Schattevoy, R. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-70L-2002) Genome Analysis, Institute of Molecular Submitted (25-70L-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany on Jul 25, 2002 this sequence version replaced gi:21622700.

Center: Institute of Molecular Biotechnology
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Db 220169 GCACACACTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 220223
                          dbsrs:STS10310
Identified using the e-PCR software (G. Schuler)"
55369 c 56129 g 58313 t
                                                                                                                                                                                                                                                                                                                                                             213 GCACACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
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Sequencing vector: pucls; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 26684 bases at least Q40
Consensus quality: 265377 bases at least Q30
Consensus quality: 265377 bases at least Q30
                                                                                                                                                                                                                DB 9; Length 228097
1e-17;
                                                                                                                                                                                                                                                                                        0; Indels
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Center clone name: CTB-415D8, SCb-332a23
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Contact: gscj-submit@genome.imb-jena.de
------ Project Information
                                                                                                                                                                                                            3.3%; Score 55; DB
100.0%; Pred. No. 1e-
tive 0; Mismatches
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RHdb: RH31992
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Homo sapiens
                                                                                                                                                                                                                                               Best Local Similarity
Matches 55; Conserv
                                                                                                          58286 a
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AF228730
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AUTHORS
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JOURNAL
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/note="single clone coverage , low quality region
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/note="single clone coverage"
66847. .66925
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/note="low quality region , CTB-415D8"
/note="single stranded/single chemistry region"
67731. .67819
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/note="low quality region , CTB-415D8"
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/note="single stranded/single chemistry 86758. 86824
/note="single stranded/single chemistry 86769
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90467. .90803
/note="single stranded/single chemistry
90700
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66957. .66958
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67550. .67655
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90465
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90741
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90742. .90745
/note="low quality region , CTB-415D8"
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/note="single clone coverage"
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Score 54; DB 9; Length 265308;

3.28;

Query Match

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Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.
AC002551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 37 (bases I to 94850)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (01-DEC-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Dec 1, 2000 this sequence version replaced gi:8576144.

Draft Sequence Produced by DOE Joint Genome Institute
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 114411)
Loftus, B.J., Kim, U.J., Sneddon, V.P., Kalush, F., Brandon, R.,
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center. Unpublished
                                                                                         Db 143104 CGTGGTGGCACACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 143157
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0
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Finishing Completed at Stanford Human Genome Center
                                     Indels
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
                   Pred. No. 3.3e-17;
Mismatches 0;
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100.0%; Pred. No. 1.3e-16;
ative 0; Mismatches 0;
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22519 c 22946 g 25486 t
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Location/Qualifiers
1. .94850
/organism="Homo sapiens"
/db_xref="taxon:9606"
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DOE Joint Genome Institute.
Direct Submission
100.0%; Pr
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             Best Local Similarity 100.
Matches 54; Conservative
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AC025275
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Streen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Campopiano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Grereira, P., Fitzhugh, W., Gage, D., Gladgan, J., Gardyna, S., Glode, S., Goyette, M., Graham, L., Gradyna, S., Glode, S., Goyette, M., Graham, L., Gradyna, S., Glode, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lander, T., Lander, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McRernan, K., Menderrs, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connoll, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talgillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Yc, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

All Schmitted (40-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC034128 149628 bp DNA linear HTG 04-MAY-2000 Homo sapiens chromosome 8 clone RP11-207E12 map 8, WORKING DRAFT SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Center code: WIBR
                                                                                                                                                                                                                                                                                                                                  Db 11842 GTGGTGGCACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 11790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhin1; Hominidae; Homo.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Craniata; Verteb 1 (bases 1 to 14962B) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo Sapiens chromosome 8, clone RP11-207E12
                                                                                                                                                                             3.2%; Score 53; DB 9; L
100.0%; Pred. No. 1.3e-16;
tive 0; Mismatches 0;
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   /db_xref="dbSTS:G02122"
101138. .101255
/db_xref="dbSTS:G02122"
1 26699 c 27271 g 30711 t
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Laborater Submission

Laborater Submission

Laborater (105-FBE-1998) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

7 (bases 1 to 11441)

8 Adams, M.D. and Loftus, B.J.

Direct Submission

8 Usbmitted (17-MAR-1998) The Institute for Genomic Research, 9712

Address all Center Dr., Rockville, MD 20850, USA

On Jan 26, 1998 this sequence version replaced gi:264242.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: mdadams@tigr.org The orientation of the sequence is five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/

Chttp://www.tigr.org/tdb/pg i/hdi.html). Genes without pepetide homology having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE/):

Location/Qualifiers

Location/Qualifiers
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/translation~"MDALESLUDEVALEGLDGLCLPALWSRLETRVPPFPLPLEPCTQ
EFLWRALATHPGISFYEEPRERPDLQLQDR"
6327. .6444
                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (19-SEP-1997) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
4 (bases 1 to 114411)
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Submitted (28-JAN-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
6 (Dases 1 to 114411)
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Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L., Deslattes Mays, A., Cao, Y., Xu, X., Kang, H.L., Mitchell, S., Etchler, E.E., Harris, P.C., Venter, J.C. and Adams, M.D. Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q Genomics 60 (3), 295-308 (1999)
                                                                                                                                                                                                  dams.M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C. Human Chromosome 16 BAC clone CIT987SK-A-951C11
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="16"

/map="16p12.1"
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/genew"A-951C1A1."
complement(<3210. .3493)
/genew"A-951C1A1."
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/gene="A-951C1A1."
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AUTHORS
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                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
Consensus quality: 145382 bases at least 030 Consensus quality: 147046 bases at least 020 Insert size: 154000; agarose-fp Insert size: 148028; sum-of-contigs Quality coverage: 4.8 in 020 bases; sum-of-contigs Quality coverage: 5.0 in 020 bases; sum-of-contigs
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of 1402 bp in length
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of 2286 bp in length
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contig of 20396 bp in length
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/note="assembly_fragment"
18926, .228a6
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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10730, .14318
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/note="assembly_fragment"
22997. .26636
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2704 4989: contig of
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10629: con
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Direct Submission

AL Submitted (16-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CBL0 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 25, 2000 this sequence version replaced gi:10933277.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human manning forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone RP11-184123 on chromosome 13 Contains AL391683.8 GI:11022494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Pred. No. 1.2e-16;
tive 0; Mismatches 0;
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1 26944 c 26014 g 47142 t
                                                                                              31115. 35710. 701e="assembly_fragment" 35811. 41703 7001e="assembly_fragment" 41804. 55435 701e="assembly_fragment" 5536. 73495 7001e="assembly_fragment" 5536. 73495 7001e="assembly_fragment." 5536. 73495 7001e=
           /note="assembly_fragment" 31115, ,35710
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/note="assembly_fragment"
95225..115620
/note="assembly_fragment"
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/note="assembly_fragment
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73596. .95124
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Les 53; Conservative
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misc_feature
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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. R11-184123 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. http://www.chori.org/bacpac/home.htm
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18266..18713
//note="LTR40b repeat: matches 4. .459 of consensus"
complement(18146..19209)
//note="match: GSS: Em:AQ053565"
//note="match: GSS: Em:AQ469501"
1879..19249
//note="match: GSS: Em:AQ469501"
18834..18913
//note="match: GSS: Em:AQ469501"
//note="match: GSS: Em:AQ469501"
//note="match: GSS: Em:AQ443749"
//note="match: GSS: Em:AQ343749"
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Mote-"HALI repeat: matches 407. .747 of consensus"

9060. .9498

/note-"Charlielb repeat: matches 51. .522 of consensus"
                                                                                                                                                                                                                                                                                                                                                  .6153 of consensus"
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/note="24 copies 2 mer tt 77% conserved"
/1316. .21316. .21480
22398. .22480
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13824. .14411
/notes"MER44C repeat: matches 147. .723 of consensus"
/notes"MLT1A1 repeat: matches 1. .359 of consensus"
15999. .16636
15090-.12 repeat: matches 710. .1436 of consensus"
16936. .170337
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                                                                                                                                                                                                                                                                                                                                                                  2452. .2804
/noter"MLTIA1 repeat: matches 12. .365 of consensus"
2814. .2924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710. .8338 Content matches 918. .1591 of consensus" (Ads. 239. .8452 Copies 2 mer at 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                            2814. .2924
/note-"L2 repeat: matches 2633. .2750 of consensus"
3367. .3867. .3867
/note-"Aux repeat: matches 1. .303 of consensus"
complement(3885. .4359)
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notes"MLT1D repeat: matches 2. .505 of consensus"
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hoten"HAL1 repeat: matches 31. .162 of consensus"
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/notee-43 copies 2 mer ta 74% conserved"
12964. .1333
/notee-NSTD repeat: matches 1. .387 of consensus"
13504. .13648
                                                                                                                                                                                                                                                                                                                                                  note "LIPA15 repeat: matches 4126.
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                                                                                                                                                                                                         /organism="Homo sapiens'
/db_xref∵"taxon:9606"
                                                                                                                                                                                                                                                                           /clone."RP11-184I23"
/clone_lib="RPCI-11.1"
11. .2005
                                                                                                                                                             Location/Qualifiers
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// CONSENSING.

/ ALOVER THANS) - INLESTING T REPEAT: MATCHES / 152. . 7286 of CONSENSUS.

25565. . 25643

/ Ancte="Lipal repeat: matches 607. . 685 of consensus."

25666. . 26287

/ Anote="Lipal repeat: matches 17. . 538 of consensus."

26294. . 28555

/ Anote="Lipal repeat: matches -764. . 1499 of consensus."

2683. . 11PA1 repeat: matches 6017. . 6145 of consensus."

Anote="Lipal repeat: matches 1499. . 5199 of consensus."

Anote="HERVE repeat: matches 1992. . 4388 of consensus."

Anote="HERVE repeat: matches 3942. . 4388 of consensus."

Anote="HERVE repeat: matches 11. . 309 of consensus."

Anote="HERVE repeat: matches 11. . 309 of consensus."

Anote="HERVE repeat: matches 1217. . 1855 of consensus."

Anote="HERVE repeat: matches 1217. . 1855 of consensus."

Anote="HERVE repeat: matches 238. . 2321 of consensus."

Anote="HERVE repeat: matches 235. . 529 of consensus."

Anote="LTR30 repeat: matches 235. . 529 of consensus."

Anote="LTR30 repeat: matches 235. . 529 of consensus."

Anote="LTR30 repeat: matches 1194. . 1311 of consensus."

Anote="LTR30 repeat: matches 1194. . 1311 of consensus."

Anote="LTR30 repeat: matches 15. . 262 of consensus."

Anote="LTR30 repeat: matches 1194. . 1311 of consensus."

Anote="LTR30 repeat: matches 15. . 262 of consensus."

Anote="LTR30 repeat: matches 1194. . 1311 of consensus."

Anote="LTR30 repeat: matches 15. . 262 of consensus."
/notes"L1PA16 repeat: matches 6071. .6157 of consensus"
22557. .22757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLTC repeat: matches 10. .461 of consensus" 42387 .42923 /note="LL repeat: matches 1733. .2239 of consensus" 44677 .45206 /note="match: GSS: Em:AQ384058" /note="match: GSS: Em:AQ384058" /note="MIR repeat: matches 28. .138 of consensus" 45703. .4600 /note="LL repeat: matches 2137. .2419 of consensus" complement(46088. .46407)
                                                                                                          7400cm." MIR repeat: matches 169. .256 of consensus" 24875. .25007
/notem."MER57-internal repeat: matches 7152. .7288 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"L2 repeat: matches 2237. .2750 of consensus"
1933. .42381
                                                         .221 of consensus"
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19097. .39178
note="MER81 repeat: matches 5. .83 of consensus"
11431. .41928
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//oote="match: GSS: Em:AQ061481"
46114. .46438
//oote="match: GSS: Em:AQ598220"
Complement(46114. .4626)
40126. .46325
//oote="match: GSS: Em:AQ388769"
46126. .46326
//oote="match: GSS: Em:AZ308449"
46154. .46390
//oote="match: GSS: Em:AZ308449"
complement(46176. .46359)
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complement(46093. .46316)
/note="match: GSS: Em:AZ098853"
complement(46093. .46273)
complement(46113. .46453)
                  22007. .22757
/note="MIR repeat: matches 25.
24392. .24478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (26-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (abses 1 to 178378) Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Homo sapiens BAC clone RP11-472F4 from 4, complete sequence
AC025821
                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 118575 GTGTGGCACACACTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGAGAAT 118627
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                      Length 168373;
                                   /note="match: GSS: Em:AQ807289"
46208. .46450
/note="match: GSS: Em:AQ017857"
46211.
/note="31 copies 2 mer at 77% conserved"
complement(46218. .46453)
/note="match: GSS: Em:AQ822390"
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Nguyen,C., Haakenson,W. and Phillips,A.
The sequence of Homo sapiens BAC clone RP11-472F4
Unpublished (2001)
3 (bases 1 to 178378)
Waterston,R.H.
Direct Submission
                                                                                                                                                                          complement(join(46222. .46326,54553.
/note="match: GSS: Em:AZ030854"
complement(46222. .46460)
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Pred. No. 1.2e-16;
/note="match: STS: Em:HSA246YG9"
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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complement(46222, .46453)
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/note="match: GSS: Em:AQ628671"
complement(46229, .46412)
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                    complement (46176
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                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 53; Conserv
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JOURNAL
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Mapping information for this clone was provided by Dr. John D. Marbherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is RP11-485611; the clone sequenced to the right is RP11-319N12. Actual start of this clone is at base position 1 of RP11-472F4; actual end is at base position 178378 of
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Data from AC023246 and AC019300 was used to finish this clone, AC025821. Polymorphisms have been identified between AC023246 (H_NH0485c11), AC019300 (H_NH0319N12), and AC025821 (H_NH0472F04). Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="4"
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/rpt_family="(T)n"
1007. .1033
/rpt_family="AT_rich"
1643. .1675
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5262. .5293
/rpt_family="(CA)n"
5975. .6059
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3424. .3457
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8272. .8314
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3657. .3679
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9396. .9522
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2725. .2848
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/rpt_family="(TA)n"

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28279. .28321
/rpt_family="AT_rich"
28548. .28934
/rpt_family="Mark"
28571. .28601
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/rpt_family~"MIR"
23475. .23509
/rpt_family~"AT_rich"
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/rpt_family="AT_rich"
[4317, 14430
                                     'rpt_family="AT_rich"
.0252. .10286
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6132. 16/12
                                                                                                      'rpt_family "AT_rich" 0695.
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4761. .14780
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5858. והחירה
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6216. .26957
                                                             rpt_family "(TTTA)n
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/rpt_family="MaLR"
18228. 18354
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1519. .21745
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rpt_family~"MalR"
            'rpt_family="(T)n"
.0019. .10056
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[251. .21272
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9668. .20131
                                                                                                                                        rpt_family~"MIR"
2510. .12533
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1727. .21759
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27.14

27.14

/rpt_family="L2"

/rpt_family="L2"

/rpt_family="L1"

28111..28219
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0493. .10522
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3599. .25659
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rpt_family~"L1"
                                                                                                                                                                              .12622
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                        .10056
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ACU23047 181438 bp DNA linear HTG 05-MAR-2001
Homo sapiens chromosome 12 clone RPI1-46H11, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 181438)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M., Vu.S. and Davis,R.W.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (07-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Vector: Milmpl8; X02513
Sequencing Vector: Milmpl8; X02513
Sequencing Vector: Milmpl8; X02513
Sequencing Vector: Milmpl8; X02513
Chemistry: Dye-Perlmer; 18 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178770 bases at least Q40
Consensus quality: 178770 bases at least Q30
Consensus quality: 180370 bases at least Q30
Insert size: 164471; agarose-fp
Insert size: 164471; agarose-fp
Insert size: 160938; sum-of-contigs
Quality coverage: 10.7x in Q20 bases; agarose-fp
Quality coverage: 9.7x in Q20 bases; sum-of-contigs.
* NOTE: This is a "working draft' sequence. It currently
* consists of 6 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC023047.19 GI:9857509
HTG: HTGS_PHASEL: HTGS_DRAFT; HTGS_FULLTQP; HTGS_ACTIVEFIN.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     DD 54164 ACACACTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAATTGCTTGAA 54216
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0
                                                                                                                                                                                                                                                                                                                           215 ACACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
                                                                                                                                                                                                                                Length 178378;
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                                                                                                                                                                                                                                                          1.2e-16;
nes 0;
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iive 0; Mismatches
                                                                                                                                                                                       /rpt_family~"(TTTTA)n"
/rpt_family…"AT_rich"
30995. .31015
/rpt_family…"(TA)n"
                                                                  31230. .31590
/rpt_family:"Malk"
32955. .33236
/rpt_family:"Malk"
33235. .33305
                                                                                                                                                                                                                                  3.28;
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Best Local Similarity 100.0
Matches 53; Conservative
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 42
AC023047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
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14683
38973
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JOURNAL
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthbria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 182908)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Burbaria, J., Benton, J., Bimage, R., Blankenburg, K., Bonnin, D.,

Burbar, G., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chowdiny, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

Davilla M.L., Davis, C., Dany, Carroll, L., Ding, Y., Dinh, H.H.,

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC127070 182908 bp DNA linear HTG 09-AUG-2002
Homo sapiens clone RP11-46H11, *** SEQUENCING IN PROGRESS ***, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 50897 GATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCT 50949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 181438;
                                                                                              7009: contig of 7009 bp in length 7109: gap of unknown length 131344: contig of 16235 bp in length 23444: gap of unknown length 18890: contig of 15446 bp in length 18990: gap of unknown length 55546: contig of 15556 bp in length 55546: contig of 16556 bp in length 103534: contig of 47888 bp in length 103634: gap of unknown length 103634: gap of unknown length 181438: contig of 77804 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI human BAC library 11"
1. .7009
/note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2%; Score 53; DB 2; L4 100.0%; Pred. No. 1.2e-16; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23445. .38890
/note="assembly_name:Contig18"
38991. .55346
/note="assembly_name:Contig19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55647. .103534 / /note="assembly_name:Contig20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103635. .181438
/note="assembly_name:Contig21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44022 a 44380 c 46244 g 46284 t
                                                                                                                                                                                                                                                                                                                                                               1. .181438
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-46H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC127070 AC127070.6 GI:22164868
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_end:SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .23344
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Best Local Similarity 100.0
Matches 53; Conservative
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55647
103535
103635
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7110
23345
23445
38891
38991
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AC127070
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Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garcia, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunarane, P., Hawes, A., Harthis, C., Harris, C., Harris, K., Harth., Havlak, P., Hawes, A., Hernandez, J., Hartis, C., Harris, C., Huber, J., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Kovah, J., Kovar, C., Kratovic, J., Kureshl, A., Landry, N., Leal, B., Louris, L., Li, J., Li, C., Lichtzey, C., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Manbiney, E., Martinel, R., Martindal, A., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Miner, G., Miner, G., Mitchell, T., Mohabbat, K., Moyen, N., Olviedo, R., Pacc, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rojas, A., Rojubokan, T., Rayton, B., Peery, J., Royler, R., Socherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutten, A., Satek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tanesy, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usman, K., Wasquez, L., Vera, W., Villalon, D., Winson, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Williams, G., Williams, G., Walliams, G., Walliams, G., Walliams, S., Narten, R., Washington, C., Wall, R., Konden, S., Murley, R., Warley, S., Warren, R., Washington, C., Wall, R., Konden, S., Warren, R., Washington, C., Wall, R., Konden, S., Warren, R., Washington, C., Wall, R., Washington, D., Walliams, G., Walliams, G.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases I to 182908)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-AUG-2002) Human Genome Sequencing Center, Department of Moliar and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 9, 2002 this sequence version replaced gi:22138209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
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Center clone name: RP11-46H11
Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 180515 bases at least Q40
Consensus quality: 180781 bases at least Q20
Consensus quality: 180936 bases at least Q20
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14682: gap of unknown length
38972: contig of 24290 bp in length
39072: gap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Center code: BCM
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FEATURES

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TITLE
JOURNAL
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TITLE
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                                                               REFERENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 303014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 3 clone RP11-264F20, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.
AC117448 AC025663
AC117448.1 GI:20127800
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 177939 GATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCT 177991
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       125 GATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCT 177
                                                                                                                                                                                                                                                                                                                    Length 182908;
                                                                                                                                                                                                                                     303 others
88137: contig of 49065 bp in length 88237: gap of unknown length 182908: contig of 94671 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                    3.2%; Score 53; DB 2; L
100.0%; Pred. No. 1.2e-16;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                  45126 g 42351 t
                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone:"RP11-46H11"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                  46295 c
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 53; Conservative
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   39073
88138
88238
                                                                                                                                                                                                                                     48833 a
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 44
AC117448/C
LOCUS
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KEYWORDS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                   Direct Submission
Submitted (04-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicinc, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced g1:7885339.
                                                    Direct Submission
Submitted (10-ARY-2002) Human Genome Sequencing Center, Department
Subjectuar and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                          1: contig of 2284 bp in length

1: gap of unknown length

1: gap of unknown length

1: gap of unknown length

1: contig of 2513 bp in length

1: contig of 2513 bp in length

1: gap of unknown length

1: contig of 3363 bp in length

1: contig of 3363 bp in length

1: contig of 3768 bp in length

1: contig of 3768 bp in length

1: contig of unknown length

1: contig of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 11552 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 11165 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 13821 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 3633 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 6266 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 4315 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length
of 6730 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 6916 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
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Drafting Center Codd: WIBR
Contact: hgsc-help@bcm.tmc.edu
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Worley, K.C.
                (bases 1 to 303014)
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Submitted (01-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Apr 2, 1999 this sequence version replaced gi:4508049.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (26-MAR-1999) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 123943)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC006208 123943 bp DNA linear PRI 01-;
Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park Cancer
Institute Human PAC Library) complete sequence.
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Worley, K.C.
Direct Submission
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Direct Submission
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DNA sequence analysis of a 1.9-Mb region on chromosome 8p11.2

Published only in Database (1999)

(bases 1 to 100000)

Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.

DIRECT Submission

Submitted (12-FB-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Database Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)

Research as a JST sequencing Team.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Phone:+81-3-5449-5372, Fax:+81-3-5449-5433,
Yusuke@hgc.ims.u-tokyo.ac.jp
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
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                        117806: contig of 18044 bp in length 117906: gap of unknown length 135151: contig of 17245 bp in length 135251: gap of unknown length 154753: contig of 19502 bp in length 154853: gap of unknown length 183456: contig of 28603 bp in length 183556: gap of unknown length 183556: qap of unknown length 183550: gap of unknown length 18356: gap of same and sam
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221574: contig of 38018 bp in length
221674: gap of unknown length
303014: contig of 81340 bp in length.
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/db_xref="taxon:9606"
/chromosome="8"
/map="8p11.2"
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genem Unigene cluster containing AJ223811, AA280976, and
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/rpt_family~"Aluy"
31632. .32081
/note="Region: qg87a10.x1 Homo sapiens cDNA AI221496"
31774. .31924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41664. .42236
/note="Region: Unigene cluster containing W95768 and
AA455370"
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                                                                                                                                                                                                                                                                                                      /rpt_family."LiMe2"
complement(24622. .24923)
/rpt_family."Alux"
24932. .2500?
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complement(34718. .35265)
/rpt_family."LiMC3"
complement/?=^.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_famlly "Alus"
complement (34083, 34777)
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27118. .27246
                                                                                                                                                                                                                                                    /rpt_family="AluSq"
complement/220cf
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/rpt_family~"LiME2"
complement (25497. .26685)
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complement.
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24993, .25290
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complement(34011. .34
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/rpt_family~"(CA)n"
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23167. 22116
  /rpt_family."AluJb"
20931. .21138
                                                                                                                                                                                                                                     AluJb"
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21525. 2172.
                                                                                                         /rpt_family="MIR"
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18522. .1847
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/complement(18554. .18661)
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/
                                                                                                                                                                                                                                                                                                                                         SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                            unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Peports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
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complement(7725...7029)
/rpt_family='Alusc"
complement(7040...7197)
/rpt_family='MIR"...197)
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complement(6668. .6724)
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Matches

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TITLE

REFERENCE AUTHORS JOURNAL

TITLE

COMMENT

DEFINITION

RESULT 47

AC010988

ACCESSION VERSION KEYWORDS

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libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                        The clone sequenced to the left is RP11-526G2; the clone sequenced to the right is RP11-247H16, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-570F4; actual end is at base position 45163 of RP11-447H16.
                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, F. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from
                                                                                                                                                                                                                                    (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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314. .8590
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790. .8882
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2109, .1214?
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                                    SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington
Noiversity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 8, 2001 this sequence version replaced gi:13270813.
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Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130069)
Sulston, J.E. and Waterston, R.
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Homo sapiens BAC clone RP11-570F4 from 2, complete sequence
AC010988
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                                            216 CACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
     Indels
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Waligorski, J., Abbott, A. and Baum, D.
The sequence of Homo sapiens BAC clone RP11-570F4
Unpublished
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Contact: sapiens@watson.wustl.edu
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  Mismatches
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Submitted (08-MAY-2001) Genome
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Direct Submission
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Lucker Submitted (12-ARP-2000) Whitehead Institute/MIT Center for Genome Submitted (12-ARP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dasses I to 142323)

Barren, B. Nutsbaun, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Lu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Marchy, M., Meldrim, J., Mender, C., Macdonald, P., Micol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Roqov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Stojanovic, N., Talamas, J., Refaye, S., Theodore, J., Topham, K., Travers, M., Vassilitov, H., Zammer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M., Direct, Submitter, Submer, S., Schup, C., Submer, S., Schup, M., Mison, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Roy, A., Wilson, B., Wyman, D., Wyman, M., Wyman, M.,
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Barren, B. Nusbaun, C. Lander, E. Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgulter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jindblad-Toh, K., Liud, G., MacLean, C., Macdonald, P., Major, J., Mathhews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
                                    Homo sapiens chromosome 11, clone CTD-2210P24, complete sequence. AC044839.16 GI:22024599
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                        1 (bases 1 to 142323)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone CTD-2210P24
10 (bases 1 to 142323)
                                                                                                                                                                                         Homo sapiens
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SOURCE
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13604. .13880
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25678. .25777
/rpt_family="MIR"
26008. .26190
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24292. .24666
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29472. .29560
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29596. .29878
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/rpt_family="MIR"
29057. .29449
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/rpt_family="L1"
17335. .17826
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31073. 21100
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20570. .20968
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27358. .27646
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18186. .18359
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14221. .15319
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5318. .15829
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15835, .15914
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15914. .16189
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19455. .19587
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22330. .22698
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28132. .28215
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13363. .13407
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Db 39182 TGGTGCCACACACACTGTAATCCCAGCTACGAGGGCTGAGGAGCAGGAGAAT 39233

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Homo sapiens chromosome 16 clone RPI1-21M24, complete sequence. AC092338
AC092338.3 GI:18481997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7349. .7474)
/note="single clone coverage"
complement(7640. .7644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="<30 qual SNGL region"
complement(7737. .7845)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7836..7841)
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complement(7912..8057)
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                                                                                                                                                                                                                                                                                               /rpt_family="MIR"
                                                                                                                                                                                                              complement(5463. .5864)
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                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alusc"
                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="MIR" (891. 7) (7)
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complement(8365..8450)
/rpt_family="MLT1H"
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Pred. No.
                                 4165. .4322
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4347. .4609
/rpt_family="AluJo"
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7405. .9768
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.0333. .10612
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10613, .1002
                                                                                                                                                                                                                                                                             /rpt_family="AluSx"
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/rpt_family="MIR3"
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                                                                                                                                                                                                                                                                                                                                                                                     complement (6640.
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.0451. .10513
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1116. .9173
                                                                                                                                                                                                                                                         complement (6008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1%;
Best Local Similarity 100.0%;
Matches 52; Conservative 0
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AC092338/C
LOCUS
DEFINITION
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                                                                                                                                                                                       AL Submission

Submitted (31-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

5 (bases 1 to 14232)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGeradd, M., Gage, D., Galagan, J., Gardham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., McCarthy, M., Maldrim, J., Meneus, L., Mihova, T., Methews, C., Macdonald, P., Major, J., Mathews, C., Norman, C., Naylor, J., Maylor, J., Morol, R., Morbu, C., Norman, C., Phunkhang, P., Pierre, M., Raymond, C., Retta, R., Seners, S., Schupback, R., Schupback, R., Schupback, R., Schupback, S., Schupback, R., Stone, S., Schupback, S., Schupback, R., Stone, S., Schupback, S., Theodore, J., Topham, K., Travers, M., Vashilev, H., Vial, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Lepeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Rettar, R., Rese, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodonc, J., Topham, K., Travers, M., Vassiliev, H., Vel. R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------------- Project information
Center project name: 18906
Center clone name: 2210_P_24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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/organism="Homo sapiens"
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2964. .304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MLT1L"
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3372. .3685
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complement(3688. .4141)
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complement(771. .872)
/rpt_family="MIR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2738. .28)
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                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                   coverage"
complement(8436..8442)
/note="<30 qual SNGL region"
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/note="<30 qual SNGL region"
10689. .10699
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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PRI 03-FEB-2002

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B., Brown, A. Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kannt, L., Karatasa, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Mcrwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Mcrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Terfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Mheeler, J., Mu, X., Direct, S., Markesion.
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Direct Submission

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases to 14357)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boquslavkly, L., Boukhgalter, B.,

Brown, A., Campoplano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Choepel, Y., Colangelo, M., Gape, D., Galagan, J., Gardyna, S.,

Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heafford, A., Horton, L., Hulme, W., Illev, I., Johnson, R.,

Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,

Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

Morbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Raymond, C., Retta, R., Raback, M., Riley, R., Schauer, S., Schupback, R.,

Scaman, S., Severti, M., Roy, A., Santos, R., Schauer, S., Theodore, J.,

Norbu, C., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Strauss, N., Subramain, A., Talamas, J., Tesfaye, S., Theodore, J.,

Viel, R., Yoo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA OA May 27, 2001 this sequence version replaced g1:14547834.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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/rpt_family Alur"
2876. .2896
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complement(4199. .4627)
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complement(4831. .4872)
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                                                                                                                                                                                                                                                                                                                    Submitted (03-30L-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute.

L. Submitted (03-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Feb 3, 2002 this sequence version replaced gi:17027254.

Sequence Quality Assessment:
This entry has been annotated with sequence quality sets.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part
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                                 Homo sapiens
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143125)
Dob Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 143125)
Dob Joint Genome Institute.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-23B7
Unpublished
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100.0%; Pred. No. 4e-16;
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Query Match 3.1%; Score 52; DB 9; Length 143577; Best Local Similarity 100.0%; Pred. No. 4e-16; Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

Search completed: February 11, 2003, 13:33:34 Job time: 8121 secs

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ligase-based sequenced determination; drug metabolism;
gene; polymorphism; ds.
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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYPDE6) gene. CYPD2D6 enzymes are involved in the metabolism of many different xenoblotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in situ spence determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's abolity to metabolise certain drugs. The present sequence is human
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The present sequence is that of the promoter region was amplified cytochrome P450 CYP2D6 gene. The promoter region was amplified by PCR from leucocyte DNA of over 50 individuals, and sequenced. By PCR from leucocyte DNA of over 50 individuals, and sequenced. By PCR from leucocyte DNA of over 50 individuals, and sequenced. Gentified. These were at: base 36 (base -1584 according to the funan Cytochrome P450 Allale Nomenclature), where the SNP was C to G, occurring at an estimated frequency where the SNP was C to G, occurring at an estimated frequency of approximately 20% in the whole population, and resulting in increased enzyme activity; control 194 (-1426), C to T, approximately 20% frequency neutral function; position 385 (-1235), A to G, approximately 20% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, rare, unknown function; and 129% (-322), T to C, rare, convention provides a metabolic ratios, and amolecular variant provides and metabolic ratios, and amolecular variant polynucleotide having G at this position is claimed (see AAH26179). The invention provides a method of diagnosing adisorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates (antidepressant, selective serotonin reuptake inhibitor, neuroleptic antidepressant, selective serotonin reuptake inhibitor, neuroleptic opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP2D6 correlation between genotype and phenotype in the CYP2D6 polymorphism. Testing for the mutation will allow the identification of intermediate metabolizers and therefore allow quantitative predictions to be made on in vivo drug metabolism capacity, thus providing a very potent to on in vivo drug metabolism capacity, thus providing a very potent to for the metabolism capacity, thus providing a very potent to charge the cyptor the correlation between generated to disconder to the cyptor of the cyptor of 
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                                                                                                   (EPID-) EPIDAUROS BIOTECHNOLOGIE
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30-JAN-2001; 2001WO-EP00954
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                                                   CCTGGTGGGGTGGGGGTGCCAGGTGTCCAGAGGAGCCCATTTGGTAGTGAGGCAGGTA 1620
                                                                                                                                                                                                                                                                       -1584 bp).
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       | GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG
                        1381 GAAGCAGGGCAAGAACCTCTGGAGCAGCCCATACCCGCCCTGGCCTGACTCTGCCACTG
                                                                             CTTTATAAGGGAAGGGTCACGCGCTCGGTGTGCTGAGAGTGTCCTGCTGGTCCTCTGTG
                                          GCAGCACAGTCAACAGCAGGTTCACTCACAGCAGAGGGCAAAGGCCCATCATCAGCTCC
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                                                                                                                                                                                                                                                                     Human cytochrome P450 CYP2D6 gene promoter (G mutation at
                                                                                                                                                                                                                                                                                      Cytochrome P450; CYP2D6; promoter; drug metabolism; diagnosis; therapy; single nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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CYP206 substrates (antiarrhythmic, beta-adrenergic receptor antagonist, tricyclic antidepressant, selective scrotonin reuptake inhibitor, neuroleptic, oplate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP206 promoter. The novel variant forms of the CYP206 gene provided by the invention provide the potential for the development of a pharmacodymaic profile of drugs for a given patient. The finding and characterization of variations in the CYP206 gene, and diagnostic tests for the discrimination of different alleles in human individuals, provide a very potent tool for improving the therapy of diseases with drugs that are targets of the CYP206 gene production, and whose metabolism is therefore dependent on CYP206 activity.

Note: The present sequence is not shown in the specification but is derived from the CYP206 promoter sequence given in the Sequence
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at position -1584 bp with increased enzyme activity. The C to G single nucleotide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1480;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.1%;
99.8%;
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(first entry)

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                                                                                                  966
ACAGCCCTGTTGCAAACAAGAAGCCATAGCCCGGCCAGAGCCCAGGAATGTGGGGCTGGGC 756
                  CAAGAGATCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGG
                                                                                                                   GAAAGGGCAAGGCCATGTTCTGGAGGAGGGTTGTGACTACATTAGGGTGTATGAGCCTA
                                                                                                                                                                                            TGGGAGCAGCCTCTGGACAGGAGTGGTCCCATCCAGGAAACCTCCGGCATGGCTGGGAAG
                                                                  TGCYCTAAGIGTCAGTGTGAGTCTGTGTATGTGTGAATATTGTCTTTGTGTGGGGTGATTT
                                                                                     TCTGCRTGTGTAATCGTGTCCCTGCAAGTGTGAACAAGTGGACAAGTGTCTGGGAGTGGA
                                                                                                                                     TGAAGTGAAGGGACCAGGCCCATGATGCCACTCATCAGGAGCTCTAAGGCCCCAGGT
                                                                                                                                                             AAGTGCCAGTGACAGATAAGGGTGCTGAAGGTCACTCTGGAGTGGGCAGGTGGGGTAGG
                                                                                                                                                                                                                                             GCTGGGAGGTGGATGGCCRGGTCCACTGAAACCCTGGTTATCCCAGAAGGCTTTGCAGGC
                                                                                                                                                                                                                                     TTCAGGAGCTTGGAGTGGGGGGGGGGGGTGACTTCTCCGACCAGGCCCCTCCACCGGCCT
                                                                                                                                                                                                                                                                     AGGGCAAAGGCCATCATCAGCTCCCTTTATAAGGGAAGGGTCACGCGCTCGGTGTGCTGA
                                                                                                                                                                                                                                                                                                                     GCCCATTTGGTAGTGAGGCAGGTATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAG
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                                      Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
ligase_based sequenced determination; drug metabolism; chromosome 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAAGGTTGTAGTGAGCCGAGATTGCATCATTGCACAATGGAGGGGAGCCACCACCTGG 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  New sequence determination oligonucleotides, useful for detecting bolymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCACTTTGGGAGCCTGAGGTGGGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCCAACATGGTGAAACCCTATCTCTACTGAAAATAYAAAAAGCTAGACGTGGTGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1338;
Pred. No. 0;
cytochrome P450 2D6 (CYP2D6) gene.
                                                                                                                                                                                                                                                                                                                                                                       Lewander T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 1; 63pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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99.68;
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                                                                                                                                                                                                                                                                                      2000GB-0021286
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                                                                                                                                                                                                                                                                                                                                                                       Andersson MK,
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                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-329785/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                              WO200218638-A2
                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                    30-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                       Risinger C,
                                                                                                                                                                                                    07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYP2D6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                 gene;
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1477 AGGCCAACCTCCTTTATAAAGGCAACGCCTCGTGTGCTGA 1536 1477 AGGCCAACGCTCTCATCTATATAAGGCAAGGGTCACGCGTGTGCTGA 1536 Qy 1537 GAGTGTCCTGCTGGTCCTGGTGCGTGGGGTGGGGTGGCTGGTGTGCCAGGGA 1596 11111111111111111111111111111111111	RESULT 5 ABQ72364 ID ABQ72364 ID ABQ72364 XX AC ABQ72364; XX AC ABQ72364; XX DT 02-SEP-2002 (first entry) XX EVAN Human CYP2D6 gene, SEQ ID NO:1 version #2. XX XX XX DE Human CYP2D6 gene, SEQ ID NO:1 version #2. XX	Key variation variation variation	variation replace (825, A) *taga e /*taga
Qy 397 TGGTGCCTGTAGTTGGGAGGCAGGGGTCCACTTGATGTCGAGACTGCAG 456 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GGAGGATGTTGTCACAGGCTGGGGCAAGGGCCTTCCGGCTACCAACTGGGAGCTCTGGGA	Qy 937 TCTGCRTGTGATCGTGCCCTGCAAGTGTGAACAAGTGTCTGGGAGTGGA 99 1111 </td <td> </td>	

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/*tag= ab
/label= PS23
/note= "Novel single nucleotide polymorphism (SNP)"
replace (2118, T)
                                                                                                                                                replace (2118, T)
/*tag= ac
/label= Post
/note= "Novel single nucleotide polymorphism (SNP)"
replace (2170, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a1
/label= PS30
/note= "Novel single nucleotide polymorphism (SNP);
together with PS30 causes the amino acid
substitution V1361"
replace (2661, C)
                                                                              /note= "Novel single nucleotide polymorphism (SNP)" replace (2067, G)
                                                                                                                                                                                                                                                                                                                                                                                    /note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution F1201"
replace (2635, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= aj
/label= pS30
/note= "Known single nucleotide polymorphism (SNP);
together with PS29 causes the amino acid
substitution Vl361"
replace (2704, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution Q151E"
replace (2716, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= an
/label= PS33
/note= "Known single nucleotide polymorphism (SNP)"
2847..3007
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/note= "Novel single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= al
/label= PS32
/note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution El55K"
                                                                                                                                                                                                                                             polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution W128R"
replace (2659, A)
                            /cons_splice= (5'site:NO, 3'site:YES) replace (2062, G)
                                                                                                                                                                                                                /*tag= ad
/label= 9825
/note= "Known single nucleotide |
replace (2179, C)
                                                                                                                                                                                                                                                                                                                                                   Ą
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                                                        /*tag= aa
/label= PS22
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/label= PS28
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/label= PS27
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/label= PS31
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/*tag= af
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/number= 4
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/number= 1
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    /*tag= k
/label= PS9
/note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution P34S"
/*tag= j
/label= PS8
/note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution VIIM"
replace (1100, T)
                                                                                                                                                                                                                                                                                                replace (1966, A)
/*tag= p
/label= PS12
/note= "Novel single nucleotide polymorphism (SNP);
replace (1974, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= u
//tag= u
/label= PS17
/note= Nooptlaingle nucleotide polymorphism (SNP);
rogether with PS18 causes the amino acid
substitution T107F"
                                                                                                                                                                    /*tag= m
/label= PS10
/note= "Novel single nucleotide polymorphism (SNP)"
replace (1843, G)
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution L91M"
replace (1984, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution H94R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= s
/label= PS15
/note= "Novel single nucleotide polymorphism (SNP)"
replace (2014, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Novel single nucleotide polymorphism (SNP);
together with PS17 causes the amino acid
substitution T107F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= y
/label= PS21
2056..2605
                                                                                                                                                                                                                                                   /note= "Known single nucleotide polymorphism (SNP)"
1884..2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution V104A" replace (2022, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution I109V" replace (2036, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label PS20
/note= "Novel single nucleotide polymorphism (SNP)"
replace (2039, T)
                                                                                                                                                           replace (1827, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           causes the replace (1997, G)
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/label= PS11
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/label= PS16
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/label= PS18
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/label= PS19
                                                                                                                                              /number= 1
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                                                                                                                                                                                                                                                                                         /number=
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/label= F
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                           ACCCTCAGGCAGCAGGAGGATGTTGTCACAGGCTGGGGCCAAGGGCCTTCCGGCTACCA
                                  122 GGAATGTGGGCTGGGGCGGCAGCCTCTGGACAGGAGGTGGTCCCATCCAGGAAACCTC
                                                                                                                   AGTGTCTGGGAGTGGACAAGAGATCTGTGCACCATCAGGTGTGTGCATAGCGTCTGTGCA
                                                                                                                                                                                                   TGTCAAGAGTGCAAGGTGAAGTGAAGGGACCAGGCCCATGATGCCACTCATCAGGAG
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  Length 6472;
               Indels
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  DB
       Pred. No. 0;
0; Mismatches
Score 907; 1
Pred. No. 0;
54.0%;
99.7%;
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       Similarity
Query Match
Best Local Sim
Matches 1057;
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Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase; antiarrhythmic; arrinythmia; adrenoreceptor antagoniat; hypertension; tricyclic antidepressant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single nucleotide polymorphism (SNP); as Y in the specification" {\sf C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Known single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution V7M" replace (1031, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Known single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution VIIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Novel single nucleotide polymorphism (SNP); given as R in the specification" replace (678, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single nucleotide polymorphism (SNP); as R in the specification"
A)
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given as Y in the specification"
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1022 CCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTGG 1061
                                                                                                                                                                                                                       Human CYP2D6 gene, SEQ ID NO:1 version #1.
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as S in t
G)
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replace (825,
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/label= PS5
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/label- PS6
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/product= "c
1001..1180
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/label~ PS7
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/label= |
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                                                                                                           DNA;
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681 ACTGGGAGCTCTGGGAACAGCCCTGTTGCAAACAAGAAGCCATAGCCCGGGCCAGAGCCCA 740
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"Novel single nucleotide polymorphism (SNP);
given as Y in the specification"
(2039, T)
                                                                                                                                                                                        /note= "Novel single nucleotide polymorphism (SNP);
given as R in the specification; together
with PS30 causes the amino acid substitution
V1361"
                                                                                   /note= "Known single nucleotide polymorphism (SNP); given as Y in the specification"
                                                                                                                                                                                                                                                                             /note= "Novel single nucleotide polymorphism (SNP);
   given as K in the specification"
                                                                                                                                                                                                                                                                                                                                                                                     /*tag= ad
/label= PS25
/note= "Known single nucleotide polymorphism (SNP);
given as R in the specification"
                                                                                                                                                                                                                                                                                                                                              /note= "Novel single nucleotide polymorphism (SNP); given as Y in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //octe= "Novel single nucleotide polymorphism (SNP);
given as S in the specification"
2606..2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Novel single nucleotide polymorphism (SNP);
given as W in the specification; causes the
amino acid substitution F1201"
replace (2635, C)
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Pred. No. 1.4e-237;
0; Mismatches 7; Indels 0
                                                                                                                                                      /cons_splice= (5'site:NO, 3'site:YES) replace (2062, G)
                                                                                                                                                                                                                                                                                                          (2118, T)
                                                                                                                                                                                                                                                                                                                                                                           (2170, A)
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                  /note= "Novel
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/label= PS23
        /label= PS20
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/label= PS22
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/label= PS27
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/label= PS28
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ilarity 99.3%;
Conservative 0
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Best Local Similarity
Matches 1010; Conserv
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                                    "Known single nuclectide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution P34S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Novel single nucleotide polymorphism (SNP);
given as W in the specification; together
with PS18 causes the amino acid substitution
T107F"
                                                                                                                                                                                                                                                                                                                                       /note= "Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution R88H"
                                                                                                                                                            /note= "Novel single nucleotide polymorphism (SNP); given as S in the specification"
                                                                                                                                                                                                                              /note= "Known single nucleotide polymorphism (SNP);
given as K in the specification"
1884..2055
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Known single nucleotide polymorphism (SNP);
given as M in the specification; causes the
amino acid substitution L91M"
replace (1984, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the mainto acid substitution H94R" replace (1997, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= s
/label= PS15
/note= "Novel single nucleotide polymorphism (SNP);
given as S in the specification"
replace (2014, C)
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given as Y in the specification; causes the
amino acid substitution V104A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Novel single nucleotide polymorphism (SNP);
given as R in the specification; causes the
amino acid substitution I109V"
(2036, C)
                                                                                                                        replace (1827, C)
 replace (1100, T)
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                                                                                                                                                                                                                                                                                                  replace (1966, A)
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/label= PS17
/note= "Novel
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/label= PS11
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GGAATGTGGGCTGGGCTGGGACCACCTCTGGACAGGAGTGGTCCCATCCAGGAAACCTC
                                         TGTGAGAGAATGTGTGCYCTAAGTGTCAGTGTGAGTCTGTGTATGTGTGAATATTGTC
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enzyme; DME-2; immunosuppressive; gene therapy; isorder; inflammatory disorder; atherosclerosis;

Human drug metabolising enzyme (DME-2) cDNA.

Human; drug metabolising enzyme;
cytostatic; autoimmune disorder;

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The present sequence is human drug metabolising enzyme (DME-2) cDNA.

Human DME and its nucleic acid molecule are useful for the diagnosis,
treatment and prevention of disorders associated with increased or
decreased expression of DME. Examples of such disorders include,
autoimmune/inflammatory disorder such as acquired immune deficiency
syndrome (AIDS), rheumatoid archritis, osteoporosis; cell proliferative
disorder such as actinic keratosis, atherosclerosis; developmental
disorder such as epilepsy, anaemia; endocrine disorder such as
acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as
acromegaly cretinism, thyrotoxicosis; pancreatic disorder such as
acromegaly disorder such as Addison's disease, obesity; qastrointestinal
disorder such as anorexia, dysphagia and hepatic tumours including
nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for
creating 'knockin' humanisca animals (pigs) or transgenic animals (mice
or rats) to model human disease. DME DNA is also in useful is gene
therapy. DME and its immunogenic fragments are useful for screening
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osteoporosis; eye disorder; hepatic tumour; Addison's disease; crctinism; rheumatoid arthitis; acquired immune deficiency syndrome; AIDS; anaemlu; developmental disorder; endocrine disorder; iritis; acromegaly; epilepsy; thyrotoxicosis; pancreatic disorder; diabetes mallitus; obesity; adenoma; gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma; actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma; cell proliferative disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing, treating and/or preventing autoimmune, inflammatory, cell proliferative, developmental, endocrine, eye, metabolic, and gastrointestinal disorders
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Yue H, Azimzai Y, Yao MG, Gan
al P, Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1593 BP; 285 A; 520 C; 470 G; 318 T; 0 other;
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                                                                                                                                                                                                                        drug
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                                                                                                                                                                      Location/Qualiflers
78..1571
                                                                                                                                                                                                                          "Human
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2000US-0177443.
2000US-0178574.
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                                                                                                                                                                                                       /product 78.15
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21-JAN-2000;
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Ring HZ, Hi
Nguyen DB,
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The nucleotide sequence of the CDNA coding region for the human auxillary cytochrome P450 species 2c6. The gene encodes a protein of 497 amino acids. The CDNA was amplified by PCR using the primers AAQ87763-6. The product was cloned into the yeast expression vectors paAH5N or pAHRR to produce the vectors p2D6 for the expression of the cytochrome P450 compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with resoluting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the
 TIGGTAGTGAGGCAGGTATGGGGCCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCA 1662
              Human cytochrome P450; amplification; PCR; primer; expression vector;
yeast NADPH-P450 reductase; safety, fusion protein; metabolite;
carcinogen; mutagen; liver metabolism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
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                                                                                                                                                                                  AA087729 standard; cDNA; 1494 BP.
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93JP-0201120.
93JP-0208279.
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(SUMO ) SUMITOMO CHEM CO LTD.
                                                                 1663 TCTTCCTGCTCCTGGTGG 1680
                                                                                    121 TCTTCCTGCTCCTGGTGG 138
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20-JUL-1993;
30-JUL-1993;
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Yabusaki Y;
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primer; expression vector;
protein; metabolite;
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"T to C change in variant 1 changes amino
acid from Cys to Arg"
                                                                                                                                                                                                                                                                                                                 Kaneko H, Komai K, Nakatsuka I, Sakaki T;
                                                                                                                                     Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds.
                                                                                                                                                                                                                                                                                                                                                                              Examples; Page 87-89; 124pp; English.
                                                                                                                                                                          Location/Qualifiers
886
                                                                              BP.
                                                                             AAQ87730 standard; cDNA; 1494
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SUMITOMO CHEM CO LTD.
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Yabusaki Y;
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AAQ87730
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Indels

Length 1494;

Query Match 3.6%; Score 61; DB 16; L Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 61; Conservative 0; Mismatches 0;

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us-09-942-310-2.oli20.rng

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Examples; Page 95-97; 124pp; English.
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/note=
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P-PSDB; AAR72378.
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Best Local Similarity
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(SUMO ) SUMITOMC
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Yabusaki Y;
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                                                                1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTG 1679
                                                                                                                                                                                                                                                 Human cytochrome P450; amplification; PCR; primer; expression vector;
yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
carcinogen; mutagen; liver metabolism; ds.
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                                                                         1 ATGGGCTAGAAGCACTGGTGCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCTGGTG 60
                                                                                                                                                                                                                                Human auxillary cytochrome P450 species 2D6 variant 2 coding region.
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                                                                                                                                                                                                                                                                                                                                                                            in variant 2 changes amino to Ser"
                                               ö
                            Length 1494;
                                              Indels
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         BP; 248 A; 509 C; 446 G; 291 T; 0 other;
                          DB 16; Ld
1.5e-13;
hes 0;
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                       3.6%; Score ...
100.0%; Pred. No. 1.5e-
**ive 0; Mismatches
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"C to G change i
acid from Thr t
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                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                       AAQ87731 standard; cDNA; 1494 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komai K,
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93JP-0201120.
93JP-0208279.
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(SUMO ) SUMITOMO CHEM CO LTD.
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                          Query Match 3.6%
Best Local Similarity 100.0
Matches 61; Conservative
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/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                           1457
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P-PSDB; AAR72377.
         Sequence 1494
                                                                                                                                                                                                                                                                                           Homo sapiens
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Yabusaki Y;
                                                                                                                                                                                                            15-NOV-1995
                                                                                                    1680 G 1680
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                                                                                                                                                                                                                                                                                                                                                                                                           EP644267-A.
                                                                                                                                                                                                                                                                                                             Key
variation
                                                                                                                       61 G 61
                                                                                                                                                                                         AAQ87731;
                                                                                                                                                                                                                                                                                                                                                           variation
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expression of the cytochrome P450 alone or p2D6R variant 2 for co-expression with the yeast NADPH-P450 reductase.

The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 (AAQ87715), 2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxiliary species and variants (AAQ87718-32), and yeast NADH-P450 reductase, either as protein or in cell extracts, and analysing the resulting metabolite to determining whether the chemical compound. The method is useful for determining whether the chemical compound. The metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTG 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer; expression vector; protein; metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human auxillary cytochrome P450 species 2D6 variant 3 coding region.
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"C to G change in variant 1 changes amino
acid from Thr to Ser"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1494;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1494 BP; 248 A; 508 C; 447 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%; Score 61; DB 16; 1
100.0%; Pred. No. 1.5e-13;
1ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds.
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1457
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SUMITOMO CHEM CO LTD.
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93JP-0208279.
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The nucleotide sequence of the CDNA coding region for the human
auxillary cytochrome P450 species 2D6 variant 3. The gene contains a
change at base 1457 from c to G as compared to the wild type sequence
(AAQ87729). This changes the amino acid residue 296 from Thr to Ser. The
cDNA was amplified by PCR using the primers AAQ87763-6. The product was
cloned into the yeast expression vectors pAAHSN or pAHRR to produce the
vectors p2D6 variant 3 for the expression of the cytochrome P450 alone
or p2D6R variant 3 for co-expression with the yeast NADPH-P450
corpound by reacting the chemical compound with recombinantly
corpound numan cytochrome P450 molecular species 1A2 (AAQ87714), 2C9
(AAQ87715), 2E1 (AAQ87716), or 3A4 (AAQ8777) or their auxillary species
cond variants (AAQ87716) or 3A4 (AAQ8777) or their auxillary species
clused protein or in cell extracts, and analysing the resulting metabolite
co assess the safety of the chemical compound. The metabolite
converted into a carcinogenic or mutagenic form through metabolism in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                               1620 AIGGGGCIAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCAICTTCCTGCTCCTGGTG 1679
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                                                                                                                                                                                                                                                                                                                                                                     Length 1494;
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                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                               Sequence 1494 BP; 248 A; 507 C; 447 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 16; I
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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100.0%; Pre-
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93JP-0201120.
93JP-0208279.
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                                                                                                                                                                                                                                                                                                                                                                                                 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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P-PSDB; AAR93182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinogenic;
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evaluation;
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This is the nucleotide sequence of the human cytochrome P450 molecular species 2D6 variant #1 which encodes a protein of 497 amino acids. The gene was amplified from a human liver derived cDNA library as 2 compared from a human liver derived cDNA library as 2 conded into the yeast expression vector pAAH5N to generate plasmid P2D6 for prodn. of the cytochrome only or into the vector PAHRR to generate control of the plasmid p2C6R for co-prodn. with the yeast NADBH-P450 reductase. The sequence is placed under control of the yeast ADH gene promoter and ctaminator. The vectors are used in amethod for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 mol. species 1A2 (AAT28380), 2C9 (AAT28381), 2E1 (AAT28382), 3A4 (AAT28383) or their variants (AAT28384-98) together with yeast NADPH-P450 reductase (either as a fused protein or as a cell carract) and analysing the resultant metabolite. The cpd. is considered carractly and analysing the resultant metabolite. The cpd. is considered serial if it is detoxified or is metabolised to a carcinogenic or "unsafe" if it is sequence 1494 BP; 248 A; 508 C; 446 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer; liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter; evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of the human cytochrome P450 molecular species 2D6 variant #2 which encodes a protein of 497 amino acids. The gene was amplified from a human liver derived cDNA library as 2 fragments of 0.4 and 0.9 kb using primers AAT26953-6. The prod. was
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                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 1.5e-13;
tive 0; Mismatches 0;
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Best Local Similarity
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cloned into the yeast expression vector pAAH5N to generate plasmid p2D6 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p2C6R for co-prodn. with the yeast NADHPH-P45D reductase. The sequence is placed under control of the yeast ADH gene promoter and terminator. The vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 mol. species lA2 (AAT28380), 2C9 (AAT28381), 2E1 (AAT28382), 3A4 (AAT28383) or their variants (AAT28384-98) together with yeast NADPH-P450 reductase (either as a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered is not detoxified or is metabolised to a carcinogenic or "unsafe" if it softentified or is metabolised to a carcinogenic cpd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of the human cytochrome P450 molecular species 2D6 variant #3 which encodes a protein of 497 amino acids. The gene was amplified from a human liver derived cDNA library as 2 fragments of 0.4 and 0.9 kb using primers AAM26953-6. The prod. was cloned into the yeast expression vector pAAH5N to generate plasmid p2D6 for prodn. of the cytochrome only or into the vector pARRR to generate the plasmid p2C6R for co-prodn. with the yeast NADH-1450 reductase. The sequence is placed under control of the yeast ADH gene promoter and
                                                                                                                                                                                                                                                                                                                                           1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTG 1679
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
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                                                                                                                                                                                                                                                                      Length 1494;
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                                                                                                                                                                                                                                                    DB 17; Len.
                                                                                                                                                                                                                                                                    Match 3.6%; Score 61; DB Local Similarity 100.0%; Pred. No. 1.5 es 61; Conservative 0; Mismatches
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93JP-0201120.
93JP-0208279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinogenic;
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20-JUL-1993;
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Matches
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terminator. The vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 mol., species 1A2 (AAT28380), 2C9 (AAT28381), 2E1 (AAT28381), 2A4 (AAT28383) or their variants (AAT28384-98) together with yeast NADPH-P450 reductase (either as a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered "safe" if it is detoxified or not rendered carcinogenic or "unsafe" if it is not detoxified or is metabolised to a carcinogenic cpd. second considered sequence 1494 BP; 248 A; 508 C; 447 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytochrome P450; amplified; PCR; polymerase chaln reaction; primer; liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter; evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                  1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGTGT 1679
                                                                                                                                                                                                                                                                                                         1 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                    DB 17; Length 1494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytochrome P450 molecular species 2D6 variant #4 gene.
                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                         1.5e-13;
                                                                                                                                                                                                                       100.0%; Pred. No. 1.5
ive 0; Mismatches
                                                                                                                                                                                                    Score 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT28398 standard; DNA; 1494 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0136053.
93JP-0201120.
93JP-0208279.
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                                                                                                                                                                                                                         Local Similarity 100.
es 61; Conservative
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20-JUL-1993;
30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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ID AAT2
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Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase; antiarrhythmia; adrenoreceptor antagonist; hypertension; tricyclic antidepressant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotyping; genotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ss.
                    /note= "Known single nucleotide polymorphism (SNP); causes the amino acid substitution V7M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Known single nucleotide polymorphism (SNP); causes the amino acid substitution VILM" replace (100, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Known single nucleotide polymorphism (SNP); causes the amino acid substitution P34S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Known single nucleotide polymorphism (SNP); causes the amino acid substitution L91M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution H94R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution V104A"
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/note= "Novel single nucleotide polymorphism (SNP)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Novel single nucleotide polymorphism (SN causes the amino acid substitution R88H" replace (271, A)
                                                                                                                                                                                                                                                                  gene coding sequence, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "CYP2D6"
                                                                                                                                                                                 standard; cDNA; 1494 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replace (263, A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace (19, A)
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/label= pS13
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/label= PS14
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/label= PS16
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/label= PS9
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                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                 Human CYP2D6
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                     02-SEP-2002
                                                                              G 1680
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                                                                                                                                                                                                          ABQ72216;
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                                                                                                                                                   RESULT 17
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yeast NADPH-P450 reductase (either as a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered "safe" if it is detoxified or not rendered carcinogenic or "unsafe" if it is not detoxified or is metabolised to a carcinogenic cpd. Sequence 1494 BP; 248 A; 507 C; 447 G; 292 T; 0 other;
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                                                                                                                                           1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTGCTG 1679
                                                                                                                      Gaps
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Human derived cytochrome; P4502D6; commercial cDNA library; yeast;
transfection; recombinant production; expression vector; mammal;
immunisation; sensitisation; antibody; determination; detection;
                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes the human derived cytochrome (HDC) P4502D6, which was obtd. from a commercial cDNA library. Yeast were transfected with an expression vector contg. the HDC cDNA, cultured and then disrupted to give a microsomal fraction. The HDC was purified from the fraction, and used to immunise and sensitise a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated. The antibody obtd. recognises HDC P4502D6, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody recognising human derived cytochrome P4502D6 - allows specific detection of cytochrome P450 species in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                        Length 1494;
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                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1494 BP; 248 A; 508 C; 447 G; 291 T; 0 other;
                                                                                     3.6%; Score 61; DB 17; I
100.0%; Pred. No. 1.5e-13;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Pages 11-13; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                      Human derived cytochrome P4502D6 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..1494
/*tag= a
                                                                                                                                                                                                                                                                                                    AAT17388 standard; cDNA; 1494 BP.
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-cross reactive; ds.
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P-PSDB; AAR81462.
                                                                                                 Best Local Similarity
Matches 61; Conserv
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP08027199-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                               G 61
                                                                                       Query Match
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AAT17388
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The invention relates to a method for haplotyping the cytochrome P450, subfamily IID, polypeptide 6 (CYP2D6) gene (ABQ7215, ABQ72364) of an individual, and also describes 29 novel polymorphic stres within the human CYP2D6 gene. The CYP2D6 gene is located on chromosome 22q13.1 and because involved in the detoxification of many drugs and contains 9 exons which encode a 497 amino acid protein (ABB09563). CYP2D6 is a mono-oxygenase involved in the detoxification of many drugs and centromental chemicals. It plays a role in the metabolism of drugs such as antiarrhythmics, adrenoreceptor antagonists and tricyclic antidepressants, and is also involved in the formation of a metabolite inked to the drug-induced lupus syndrome observed with procainanide. Variations in CYP2D6 activity or expression may also influence an individuals susceptibility to environmentally-linked diseases, and it has been demonstrated that CYP2D6 activity may be involved in the pathogenesis of Parkinsons's disease, with individuals with a less active condition. CYP2D6 nucleic acid sequences are useful in studying the expression and drug-induced lupus syndrome) or which are metabolised by CYP2D6. The treatment of CYP2D6 associated diseases (e.g., hypertension, atrial and ventricular arrhythmias, parkinson's disease, and drug-induced lupus syndrome) or which are metabolised by CYP2D6. Of polymorphisms on the biological activity of CYP2D6, polymorphisms on the biological activity of CYP2D6, polymorphisms on the biological activity of CYP2D6. Polymorphisms on the biological activity of CYP2D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel genetic variants of Cytochrome P450, Subfamily IID, Polypeptide 6 isogenes, useful for improving efficiency and reliability in drug development for treating hypertension, arrhythmias and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTG 1679
                                                                              /note: "Known single nucleotide polymorphism (SNP); causes the amino acid substitution S486T" replace (1489, T)
                                                                                                                                                             /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution R497C"
               /noter "Novel single nucleotide polymorphism (SNP)"
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                                replace (1457, C)
                                                                                                                                                                                                                                                                                                                                                                              Choi JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; Fig 2; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                GENA-) GENAISSANCE PHARM INC
                                                                  PS41
                                                                                                                                                 PS42
   /label- PS38
                                                                                                                                                                                                                                                                               09-NOV-2001; 2001WO-US47396.
                                                                                                                                                                                                                                                                                                               09-NOV-2000; 2000US-247943P.
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Rounds E;
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                                                                                                                                                                                                               WO200238589-A2
                                                                                                                                                                                                                                                                                                                                                                                Anastasio AE,
                                                                                                                                                                                                                                                                                                                                                                                                 Petersen N,
                                                                                                                                                                                                                                               16-MAY-2002
                                 variation
                                                                                                                variation
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   /note- "Novel single nucleotide polymorphism (SNP);
generates a premature stop codon (R344STOP)"
replace (1083, C)
                                             /notew "Novel single nucleotide polymorphism (SNP); together with PS18 causes the amino acid substitution T107F"
                                                                                                                                                                                                                                             /note~ "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution I109v"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Novel single nucleotide polymorphism (SNP);
together with PS30 causes the amino acid
substitution V1361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //note- "Known single nucleotide polymorphism (SNP);
together with PS29 causes the amino acid
substitution V1361"
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    causes the amino acid substitution Q151E"
replace (463, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /notes Novel single nucleotide polymorphism (SNP); causes the amino acid substitution E155K" replace (696, C)
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    causes the amino acid substitution V338M"
replace (1030, T)
                                                                                                                                            /note "Novel single nucleotide polymorphism (SNP); together with PS17 causes the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution F1201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note: "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution W128R"
                                                                                                                                                                                                                                                                                                                                                                                            /note∵ "Known single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                           /note∵ "Novel single nucleotide polymorphism (SNP)
                                                                                                                                                                         substitution T107F"
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                                                                                                                                                                                                                                                                             (333, C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (406, A)
replace (319, T)
                                                                                                                                                                                              (325, G)
                                                                                                                                                                                                                                                                                                                                              (336, T)
                                                                                               (320, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (408, C)
                                                                                                                                                                                                                            PS19
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               /*tag~ j
/label~ PS17
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/label~ PS18
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/label= PS29
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/label~ F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification of cytochrome P450 enzyme bufuralol-1'-hydroxylase - as indication of extensive-poor metaboliser pheno:types, important for drug dosage
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/note= "G(506) is deleted; results in frameshift
c.f. genomic P450II2D sequence"
                                                                                                                                                                                                                                                                                                                                                                                c. rc.f. C(383) in Gonzalez et al., (1988)
Nature, 331, 442-445."
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                                                                                                                                                                                                                 dbl; Extensive metaboliser/poor metaboliser; EM/PM; ss.
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                                                                                                                                                                                                                                                                                                                                                         note= "first 64 bases of intron 1"
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                                                                                                                                                                                         Debrisoquine hydroxylase variant "a".
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                             AAQ12893 standard; cDNA; 1586 BP.
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                          1680 G 1680
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                                                     1620 AIGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTG 1679
                                    Gaps
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                                                                    0;
             Length 1586;
DB 12; المصرة. 1.5e-13; من 1.5e-13; O; Indels
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   3.6%; Scc...
100.0%; Pred. No. 1...
'.. 0; Mismatches
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ID ABA16633 standard; DNA; 13836 BP.
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2000US-0180628.
2000US-0184664.
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2000US-0224519.
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Best Local Similarity 100.
Matches 61; Conservative
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02-MAR-2000;
16-MAR-2000;
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07-JUN-2000;
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14-JUL-2000;
26-JUL-2000;
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11-JUL-2000;
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2000US-0244617.
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2000US-0229287.
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2000US-0246478.
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2-OCT-2000;
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PR 17-NOV-2000; 2000US-024211.

PR 17-NOV-2000; 2000US-024221.

PR 17-NOV-2000; 2000US-024225.

PR 17-NOV-2000; 2000US-024225.
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Query Match 3.2%; Score 53; DB 22; Length 13836; Best Local Similarity 100.0%; Pred. No. 9.9e-11; Matches 53; Conservative 0; Mismatches 0; Indels 0;

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RESULT 20

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2000US-0198123.
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20000S-0226681.
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11-JUL-2000; 2000US-0217496.
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                                     17-JAN-2001; 2001WO-US01354
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19-MAY-2000; 2
07-JUN-2000; 2
28-JUN-2000; 2
30-JUN-2000; 2
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16-MAR-2000;
17-MAR-2000;
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22-AUG-2000
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29-SEP-2000;
           The invention relates to a DNA array for identifying cancer related genes. The DNA array comprises: (a) statistically significantly higher results of over 10% in homology search of a DNA molecule describing different genes or a complementary DNA (cDNA); (b) statistically significantly higher results (p value) of over 10% in homology search with human Alu sequence; (c) difference of melting temperature of the DNA fragment and hybridisation temperature at 30 degree C or less; (d) the DNA fragment prepared by immobilisation of a DNA short sequence with short repetition higher order structure; and (e) the DNA fragment without short repetitive sequence. The array is used in elucidation of the action mechanism of anticancer agents. ABK92989-ABK93090 represent human cancer related genes and associated primers of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A DNA array that observes the expression of cancer related genes is useful for the elucidation of the action mechanism of anticancer agents % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\}
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                                                                                                                                                                                                                                                    Human; cancer; DNA array; gene expression analysis; gene; ss.
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                                                                                                                                                                                          cDNA encoding human cytochrome p450 dbl
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                       ABK93054 standard; cDNA; 303 BP
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02-0CT-2000;
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03-0CT-2000;
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AAK54951 to AAK64702 encode the human immune/hacmatopoictic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polyuucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce to cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer human immune/haematopoietic-darived cells. AAK64703 cancers and reast human immune/haematopoietic antigen genomic cancers the present human immune/haematopoietic antigen genomic represent sequences trom the present invention. AAK64942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                      Disclosure; SEQ ID NO 32418; 3071pp + Sequence Listing; English.
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100.0%; Pred. No. 1.5e-09;
Live 0; Mismatches 0; Indels (
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AAK77607 standard; DNA; 6801 BP.
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18-APR-2000;
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26-JUL-2000;
14-AUG-2000;
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22-AUG-2000,
23-AUG-2000,
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 32419; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
complement the patients own produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent.

Children and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703

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to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                        Gaps
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                                                                                                                                                 218 CACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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Isolated is is used in

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RESULT 24 AAL36886,

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Ruben SM;

Barash SC,

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(HUMA-) HUMAN GENOME SCI INC

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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. broast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointesinal tract, liver, lung, or urogenital; (b) immune characters e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collitis; (c) cardiovascular discrets such as myocardial isohaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.

Dersitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                   Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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Pred. No. 2.7e-09;
                                                                                                                                                       Example 2; SEQ ID NO 3251; 781pp + Sequence Listing; English.
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Best Local Similarity
                                  WPI; 2001-451937/48
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                Gaps
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cytostatic; gene therapy; vaccine; metastasis; ds.
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   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with lamppropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
complement the patients own produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
co AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 36984; 3071pp + Sequence Listing; English.
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Amountain the partients and panel numbers, and an antitude of antitude of antitude of antitude of antitude of antitude of activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and transment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) colynucleotides may be used to produce the secreted (1), by inserting polynucleotides may be used to produce the secreted (1), by inserting the call in proteins and polynucleotides may be used to protect of diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. Akk64703 to AAK87694 represent human immune/haematopoietic antigon genomic sequences from the present invention. Addition of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; antiinflammatory; arti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirhaumatic; hepatotropic; cerebroprotective; antinflammatory; antiallergic; antidiabetic; antilocar; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)
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                                                                                                                                                                                                             Disclosure; SEQ ID NO 36983; 3071pp + Sequence Listing; English.
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Pred. No. 2.6e-09;
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                                                       Ruben SM;
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                (HUMA-) HUMAN GENOME SCI INC.
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2000US-0186350.
2000US-0189874.
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                                                       Barash SC,
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Best Local Similarity
                                                                                            WPI; 2001-483426/52
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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                                                       Rosen CA,
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13-OCT-2000; 2000US-0249940.
20-OCT-2000; 2000US-0241785.
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20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-024677.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246528.
17-NOV-2000; 2000US-0246528.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249219.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249219.
17-NOV-2000; 2000U
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SM; Rosen CA, Barash SC, Ruben (HUMA-) HUMAN GENOME SCI INC

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 13036; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating

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2000US-0225267.
2000US-0225268.
2000US-0225270.
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2000US-0227009.
2000US-0228924.
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2000US-0225757.
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08-NOV-2000
          medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antipagnists are useful.)

The nucleic acids, proteins, antibodies and (antipagnists are useful.)

In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal net of the sequence data for this patent did not form part of the print of a perilical of the control of the event of the properties of the control of th
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2000US-0205515.
2000US-0209467.
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19-MAY-2000;
07-JUN-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The higgorisis, treatment and prevention of: (a) cancer, e.g. breast in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and and parastic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 13038; 1701pp + Sequence Listing; English
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2000US-0249210.
2000US-0249211.
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2000US-0246526.
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2000US-0246532.
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2000US-0249265.
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2000US-0249300.
2000US-0250391.
2000US-0251160.
2000US-0251988.
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                        08 - NOV - 2000;
17 - NOV - 2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                        Gaps
                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20153
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Pred. No. 1.7e-08;
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100.0%; Pred. No. 1...
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2000US-019123.
2000US-020515.
2000US-0209467.
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2000US-0230438.
2000US-0231242.
2000US-0231243.
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14-SEP-2000;
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21-SEP-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (1)

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
creatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
creatment be prectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
csupplement the patients own production of (1). Additionally, (1)
copolynucleotides may be used to produce the secreted (1), by inscrting
the nucleic acids into a host cell and culturing the cell to express the
correction. (I) proteins and polynucleotides may be used to provent,
diagnose and treat immune/haematopoietic-related diseases, especially
concerns and cancer metastases of haematopoietic antigen genomic
characteristic from the present invention. AAK84942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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06-DEC-2000; 2000US-0251868.
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RESULT 31
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AC AAK77234;
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2000US-0249300
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     14 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 22 - SEP - 2000; 25 - SEP - 2000; 26 - SEP - 2000; 27 - SEP - 2000; 29 - SEP - 2000; 20 - CCT - 2000; 20 - C
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08-DEC-2000)
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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L7-NOV-2000;
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      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32046.
                                                                                                                                                                                                                                                                                                                          20000us - 0190076
20000us - 0190076
20000us - 0209467
20000us - 0209467
20000us - 0216486
20000us - 0216486
20000us - 0216480
20000us - 0217486
20000us - 0217487
20000us - 0218290
2000us - 0220964
2000us - 0225213
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2000US-0180628.
2000US-0184664.
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2000US-0225759.
2000US-0226279.
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2000US-0229287.
2000US-0229343.
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20000S-0229513
20000S-0229513
20000S-0230437
20000S-0231242
20000S-0231243
20000S-0231413
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2000US-0189874.
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2000US-0225447
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2000US-0227009
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07-NOV-2001 (first entry)
                                                                                                                                              WO200157182-A2
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44-FEB-2000)

52-MAR-2000)

15-MAR-2000)

16-MAR-2000)

17-MAR-2000)

18-MAY-2000)

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14-MG-2000)

15-MG-2000)

16-MG-2000)

16-MG-2000)
                                                                                                               Homo sapiens.
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WO200175093-A1.

11-OCT-2001

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                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
ce expression by rectifying mutations or deletions in a patient's genome
control of the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
consultations and polynuclectides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
connects and cancer metastess of haematopoietic-related diseases, especially
connects and cancer metastesses of haematopoietic antigen genomic
connects and cancer metastesses of haematopoietic antigen genomic
connects from the present invention. AAK54942 to AAK84950 and AAM82169
ce represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                  : acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; cytoklne; cell proliferation; cell differentiation; antinflammatory; stem cell growth factor; activin; inhibin; cancer; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; huntington's disease; spinal cord disorder; head trauma; stroke; myeloid cell disorder; lymphoid cell disorder; platelet disorder; thrombocytopaenia; stem cell disorder; splatelet disorder; thrombocytopaenia; stem cell disorder; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; fibrosis; reperfusion; immune disorder; severe combined immunodeficiency; infection; autoimmune disorder; severe combined immunodeficiency; infection; autoimmune disorder; asthma, coaquiation disorder; haemophilis; sepsis; nephritis; inflammatory bowel disease; food supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                         Disclosure; SEQ ID NO 32046; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 1627; 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 CCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1627 BP; 527 A; 333 C; 286 G; 481 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel cytokine encoding cDNA 790CIP2C_7 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%; Score 48; DB 100.0%; Pred. No. 1.1 tive 0; Mismatches
                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AASS9828 standard; cDNA; 776 BP.
                                                                                   (HUMA-) HUMAN GENOME SCI INC
                           2000US-0251990.
2000US-0254097.
                                                        2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0
                                                                                                                                                                     Nucleic acids encoding
                                                                                                               Barash SC,
                                                                                                                                         WPI; 2001-483426/52.
08-DEC-2000;
                           08-DEC-2000;
                                                        05-JAN-2001;
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                                                                                                                                                                                               metastasis
                                                                                                                CA,
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                                                                                                                Rosen
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The invention relates to isolated human polypeptides (which may be cytokines) and the polynucleotides encoding them. The protein is useful cort identifying a compound which binds to it (e.g. modulators, agonists and antagonists). The polynucleotides are useful as an array for mismatch detection. The proteins and nucleic acids are useful as nutritional sources or supplements. The protein exhibits exhibits activity relating to cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity, immune stimulating or immune suppressing and activin or inhibin related activities. The proteins (and antibodies raised against them) and nucleic acids are therefore useful in the diagnosis and treatment of diseases and disorders such as cancer, central and peripheral nervous system diseases and neuropathies, central and peripheral nervous system diseases and neuropathies, at lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders, thrombooytopaenia, stem cell disorders, allosted in tissue cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, inciations, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or ericating osteoporosis, various immune disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, diabeter molitics and disorders including autoimmune disorders including area.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence encodes a novel protein of the
                                                                                                                                                                                                                                                                                                                                                                                                              ang J, Xu C;
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and nucleic acids, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone degenerative disorders, cancer and promoting wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J,
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100.0%; Pred. No. 2.8e-08;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      , Ren F, Zhang J, W
Goodrich RW, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1527 GGTGTGCTGAGAGTGTCCTGCTCGTCCTCTGTGCCTGGTGGGGTGG 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 188-189; 336pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang D,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Asundi V, Zhou P,
Zaho QA, Chen R, W
                                                                                                         23-AUG-2000; 2000US-0649167.
22-SEP-2000; 2000US-066680.
23-OCT-2000; 2000US-0695618.
30-NOV-2000; 2000US-0728711.
14-MAR-2001; 2000US-0728711.
30-MAR-2001; 2001WO-US10484
                                                                          2000US-0540217
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P-PSDB; AAU68536.
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                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                          31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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ID AAA9
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AC AAA9
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AAA96363;

us-09-942-310-2.oli.20.rng

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Gaps

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132 TGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCC 176

Length 50000;

Score 45; DB 21; Pred. No. 7.8e-08;

2.7%; Scot. 100.0%; Pred. No. ... 0; Mismatches

Local Similarity 100. hes 45; Conservative

Sequence 50000 BP; 14521 A; 9882 C; 11191 G; 14406 T; 0 other;

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Two human bacterial artificial chromosome (BAC) clones that included and flanked the human CTLA-4 locus were cloned and sequenced. The sequence data was assembled into a contiguous sequence that is presented in AAA9563-68. AAA95636-64 comprise BAC clone 22700, and AAA96365-68 comprise BAC clone 22608. The sequences contain polymorphic microsatellite repeat (PMR) sequences. The specification describes a method for determining the predisposition of a human subject to develop autoimmune disease. The method comprises detecting a PMR sequence in the 1028, ICOS gene or CTLA4 gene of the human costimulatory receptor gene locus (hCGRL). PMR sequences vary in length among individuals and can be amplified to generate products that differ in size. These products can then be detected by rapid and convenient high resolution processes. The method is useful for determining the predisposition of insulin dependent attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method is useful for determining the predisposition of insulin-dependent diabetes mellitus (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism, myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis, rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy. PMR sequences within hCRGL are useful as markers in a variety of assays and in the field of forensic medicine, disease diagnosis and human genome mapping.
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Db 14836 TGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCC 14792
                                     Query Match
                                                                                                                                                                    AAC89560/c
                                                                Matches
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                              Polymorphic repeat microsatellite sequences present in the CTLA4 locus.
                                                                    ICOS gene; CTLA4 gene; COSTIMULATORY ECCEPTOR GENE 100013; CGRL; Lupus; insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy; Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma; thyroiditis; postpartum thyroiditis; rheumatoid arthritis; Hashimoto's disease; coeliac disease; ss.
                                                          disease; polymorphic microsatellite repeat; PMR; CD28 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining predisposition of humans to develop autoimmune disease involves detecting polymorphic microsatellite repeat sequence within
                                                                                                                                                                                          5722..5746
/*tag= a
/note= "sara41/42 microsatellite repeat"
                                                                                                                                                                                                                                                    /note= "sara43/44 microsatellite repeat"
[9911..19956
                                                                                                                                                                                                                                                                                         'note = "PW210/211 microsatellite repeat"
33904..23957
                                                                                                                                                                                                                                                                                                                                     noté= "sara45/46 microsatellite repeat"
27689..27780
                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/note= "saral7/18 microsatellite repeat"
                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= f
/note= "saral9/20 microsatellite repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human costimulatory receptor gene locus
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 67-82; 160pp; English.
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       (first entry)
                                                                                                                                                                                                                                   6550..6597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200056856-A2
     08-FEB-2001
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                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2000
                                                          Autoimmune
                                                                                                                                                                                           satellite
                                                                                                                                                                                                                                    satellite
                                                                                                                                                                                                                                                                           satellite
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Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C; HDAC-D; cell cycle; tumourigenesis; cancer; inhibitor; antisense;

gene therapy; ds

WO200071703-A2. Homo sapiens

30-NOV-2000

Human histone deacetylase HDAC-D coding sequence.

(first entry)

08-MAR-2001

AAC89560;

AAC89560 standard; DNA; 122186 BP

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                                            The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-2, HDAC-5, HDAC-0. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              identifying which histone deacetylase is involved in a neoplasia.
                                                                                                                                                                                                     Sequence 122186 BP; 29016 A; 31077 C; 32425 G; 29668 T; 0 other;
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                        Length 122186;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                              Db 35936 CACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 35893
                                                                                                                                                                                                                                                                                                                                          216 CACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT
                                                                                                                                                                                                                                                                        100.0%; Pred. No. 1.6e-07; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                    Score 44;
Pred. No.
Disclosure; Page 89-125; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK83459 standard; cDNA; 128978 BP.
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                      Query Match
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ID ABK8345
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AC ABK8345
XX
DT 14-AUG-
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jo.

Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal

Besterman JM;

Li Z,

Macleod AR,

WPI; 2001-016407/02.

03-MAY-2000; 2000WO-IB01252.

99US-0132287.

03-MAY-1999;

(METH-) METHYLGENE INC.

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated the expression level to an expression level in an unactivated of GCA. Also included are modulating (MS) GA by contacting GCA with an agent that alters the expression of at least one gene in GS: (2) screening (MS) for an agent capable of modulating GCA or an inflammation (especially chord of a least one gene in GS: (2) screening (MS) for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially cronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammation; for the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting an allergic of modulating GCA, M3 is useful for screening an agent capable of modulating GCA prefectally in an inflammation (especially chronic) in a tissue, an allergic exposure of a subject to a pathogen or sterile of anymistic response in a subject of a pathogen or sterile of anymistic and anymistic anymistic and anymistic anymistic anymistic anymistic anymistic any
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                                                                                                        Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; andlt respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
Human cDNA differentially expressed in granulocytic cells #30.
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Sequence 128978 BP; 35134 A; 31020 C; 29358 G; 33466 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                   ChKl protein; SQ/TQ motif; isoelectric point; cell cycle progression; ds; nuclear localisation signal; DNA replication checkpoint; benign neoplusm; cell proliferative disorder; malignant neoplasm; human; claspin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Claspin polypeptide specifically interacting with ChKI protein useful for identifying compound that modulates cell cycle progression and for treating cell proliferative disorder like neoplasm .
                                         Gaps
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     Length 128978;
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                                                                                          Db 102674 CACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 102631
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                                                                      216 CACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT
     DB 24; I
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Pred. No. 4.3e-07;
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                                       Mismatches
     Score 44;
Pred. No.
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2.6%;
100.0%; Pre
                                                                                                                                                                                            ABK52612 standard; DNA; 58837 BP
                                                                                                                                                                                                                                                                                                    Human Claspin genomic sequence.
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                                       Conservative
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Matches 43; Conservative
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Query Match
Best Local Similarity
Matches 44; Conserv
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2000US-0232397.
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2000US-0234998.
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       Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antiannemic; antiarthritic; cancer; antiinflammatory; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                  Human nervous system related polynucleotide SEQ ID NO 9675
                                                                                                                                                                                                                                                                                                            2000US-0179065.
2000US-0186628.
2000US-018664.
2000US-018974.
2000US-0199076.
2000US-0199076.
2000US-020515.
2000US-020515.
2000US-0215135.
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                                        (first entry)
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
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06-SEP-2000;
08-SEP-2000;
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26-JUL-2000;
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WPI; 2001-662795/76.
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25-MAY-2000;
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18-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                   Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 9675; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             irom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 CACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1 CACCTGTAATCCCAGCTACGTAGGAGGCTGAGGCAGAGAAT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 245 BP; 48 A; 76 C; 59 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
2.5%; Score 42; DB 22; Best Local Similarity 100.0%; Pred. No. 2.5e-06; Matches 42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 60137.
                                                                                                                                                                                      Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV60146 standard; cDNA; 287 BP
                                                      200005-0251479.
200005-0251856.
200005-0251868.
200005-0251869.
                                                                                                    2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                               2000US-0251988.
2000US-0256719.
                       1000US-0251030
                                                                                                                                        05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                useful for preventing, cancers and metastases
                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                           WPI; 2001-541565/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200160860-A2
                              05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2002
                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV60146;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 recerecegrecerearecerateareceaecaerrreceae 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 287 BP; 49 A; 85 C; 45 G; 108 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 11474; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 13368.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                   2000US-207454P.
2000US-211314P.
2000US+219007P.
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                                                                             2000US-183319P.
2000US-189862P.
20-FEB-2001; 2001WO-US05171
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                                                                                                                                                                                                                                                                                  2000US-255281P
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Matches 42; Conservative
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Claim 1; SEQ ID 8121; 489pp; English.
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ABV20089
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                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and extivity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or I cell expressing
                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                          Claim 1; SEQ ID NO 13368; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 387; 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian cancer related cDNA clone SEQ ID NO:8121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 TGGGTGCGGTGCCTATAATCCCAGCACTTTGGGAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 TGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 64
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 387 BP; 93 A; 99 C; 78 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.5%; Score 42; DB 100.0%; Pred. No. 2.3 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL85143 standard; cDNA; 397 BP
                                                                   Liu C, Drmanac RT;
 28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-2001; 2001WO-US17756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0
                                                                                             2001-514838/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                         (HYSE-) HYSEQ INC
                                                                                                           P-PSDB; AA013377
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                                                                                                                                                                  disorders
                                                                   Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL85143;
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II).

(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PGN). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (III) is useful in design and preparation of robozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a contacting to the contacting and contacting a contacting and contacting a contacting a contacting a contacting and contacting a contacting a contacting a contacting a contacting a contacting a contacting and contacting a contacting a contacting and contacting a contacting and contacting a contacting a contacting and a contacting a contacting and a contacting a contacting a contacting and contacting and contacting a contacting a contacting a contacting and a contacting and a contacting and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 24; Length 397;
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 397 BP; 100 A; 104 C; 84 G; 107 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 CACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 CACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 98
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100.0%; Pred. No. 2...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV20089 standard; cDNA; 584
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2000US-207454P.
2000US-211314P.
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2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200160860-A2.
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09-JUN-2000;
18-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        techniques
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WO200022430-A2
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30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frazer CM,
                                                                                                                                                                                                                                                                                                                                          AAA81674;
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                          AAA8167
                                                                                                                                                                                                                                                                                              RESULT
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                                           The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                  (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogent potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmucogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                       (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                   Gaps
for detecting presence of prostate cancer, stage of prostate cancer

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                           Length 584;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                    Sequence 584 BP; 139 A; 152 C; 129 G; 163 T; 1 other;
                                                                                                                                                                                                                                                                                                                    242 TGGGTGCGGTGGCTCATAATCCCAGCACTTTGGGAG 283
                                                                                                                                                                                                                                                                                                       70 regerecercerectarancecageactriegeag 111
                                                                                                                                                                                                                                                         DB 23; L
2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate expression marker cDNA 25910.
                                                                                                                                                                                                                                                         Ouery Match 2.5%; Score 42; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 42; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                       Claim 1; Page 3276; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 5240; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                       ABV25919 standard; cDNA; 584 BP
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2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                                                                                                   cancer in a patient;
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09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
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                                                                                                                                                                                                   patient;
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(a) assessing whether a patient is arrithment in a patient;
(b) monitoring the progression of prostate cancer in a patient;
cancer in a patient;
(d) assessing the efficacy of a test compound to inhibiting prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis, Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81266 to AAA81303 and AAA825620 to AAA825663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 the AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis ManB polynucleotide ORF sequences, which are all used in the exemplification of the present

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

specification or its complement. (I) is useful for:
(a) assessing whether a patient is affilted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
(c) assessing the efficacy of a test compound to inhibit prostate
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Ratti G, Scarselli M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 584 BP; 139 A; 152 C; 129 G; 163 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TGGGTGCGGTGGCTCATAATCCCAGCACTTTGGGAG 283
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Pred. No. 2.2e-06;
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99US-0132068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Conservative
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Rappuoli R, Pizza M;
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2000US-0228924.
2000US-0229287.
2000US-0229343.
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2000US-0230437
2000US-0230438
2000US-0230438
2000US-0231243
2000US-0231244
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2000US-0229345.
2000US-0229509.
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2000US-0237039.
2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0225759
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2000US-0225757
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2000US-0227009
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2000US-0232080.
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2000US-0241786.
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2000US-0241808.
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2000US-0244617
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2000US-0246477
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2000US-0246526.
                                                      14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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14-SEP-2000;
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26-SEP-2000;
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29-SEP-2000;
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02-OCT-2000;
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13-OCT-2000;
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                     invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes; particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
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0
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1 Similarity 100.0%; Pred. No. 1.9e-06;
42; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                         Sequence 1180 BP; 375 A; 205 C; 304 G; 296 T; 0 other;
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2000US-0186350
2000US-0189074
2000US-0190074
2000US-0190123
2000US-0209467
2000US-0209467
2000US-021886
2000US-0215135
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2000US-0217487.
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Best Local Similarity
Matches 42; Conserv
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18-APR-2000;
19-AAR-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-JUL-2000;
14-JUL-2000;
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24-FEB-2000;
02-MAR-2000;
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Gaps

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Indels

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Human; reproductive system related antigen; reproductive system disorder;
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                                                                              1226 TGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 1267
                                                          70 TGGGTGCGGTGCCTCATGCCTATAATCCCAGCACTTTGGGAG 111
100.0%; Pred. No. 1.5e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                            AAL03263 standard; DNA; 24977 BP
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2000US-0189874.
2000US-0190076.
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2000US-0205515.
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2000US-0224518.
2000US-0224519.
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2000US-0216880
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2000US-0217496
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  Best Local Similarity 100.
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                    cancer; gene therapy; ds
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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18-AUG-2000;
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19-MAY-2000;
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14-AUG-2000;
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14-AUG-2000;
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22-AUG-2000;
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                                                                                                                                                                                                                                AAL03263;
                                                                                                                                                    RESULT 45
AAL03263
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                                                            å
                                                                                                                                                                                                                                  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
complynicateotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
concerns and cancer metastases of haematopoletic-related diseases, especially
concerns and cancer metastases of haematopoletic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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2000US-0246611.
2000US-0246613.
2000US-0249207.
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17-NOV-2000;
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06-DEC-2000;
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2000US-0230437 2000US-0230438

DB 22; Length 5690;

2.5%; Score 42;

Query Match

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2000US-0233065.
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2000US-0241787
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2000US-0249210.
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08-SEP-2000, 08-SEP-2000, 08-SEP-2000, 08-SEP-2000, 08-SEP-2000, 08-SEP-2000, 14-SEP-2000, 14-SEP-2000, 14-SEP-2000, 14-SEP-2000, 14-SEP-2000, 14-SEP-2000, 14-SEP-2000, 25-SEP-2000, 25-SE
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
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02-0cT-2000;
02-0cT-2000;
13-0cT-2000;
13-0cT-2000;
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17 - NOV - 2000;
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-NOV-2000;
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-NOV-2000;
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17-NOV-2000;
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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2000US-0249245.
2000US-0249264.
2000US-0249297.
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2000US-0251030.
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2000US-0254097.
2001US-0259678.
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2000US-0186350.
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      PRANTHER SECONDARY SECONDA
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2000US-0241221 2000US-0241785-2000US-0241786-2000US-0241808-2000US-0241809-2000US-0241809-2000US-024617-2000US-024617-2000US-0246474-2000US-0246476-

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20000S-0215135.
20000S-0215135.
20000S-021547.
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Disclosure; SEQ ID NO 8476; 1297pp + Sequence Listing; English. Barash SC, Ruben SM, 2000US-0246528. 2000US-0246532. 2000US-0246609. 2000US-0246610. 2000US-0246611. 2000US-0246613. 2000US-0249207. 2000US-0249208. 20000S-0249213 20000S-0249213 20000S-0249214 20000S-0249216 20000S-0249216 20000S-0249217 20000S-0249218 20000S-024924 20000S-024926 2000US-0250160. 2000US-0250391. 2000US-0251030. 2000US-0251198. 2000US-025719. 2000US-0251876. 2000US-0249209. 2000US-0249210. 2000US-0249211. 2000US-0251868. 2000US-0251869. 2000US-0251989. 2000US-0251990. SCI INC 2001US-0259678 2000US-0254 (HUMA-) HUMAN GENOME WPI; 2001-465570/50 13-0CT-2000;
20-0CT-2000;
20-0C Rosen CA,

Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used

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in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                  Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of 973 mean testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and assatcolitestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
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                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                              Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                      Gaps
                                                            used in preventing, treating or ameliorating a medical condition
                                                                                  Disclosure; SEQ ID NO 5950; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                        2.5%; Score 42; DB 22; Length 24983;
100.0%; Pred. No. 1.2e-06;
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                                                                                                                                                                                 Sequence 24983 BP; 7104 A; 5397 C; 5409 G; 7073 T; 0 other;
                                                                                                                                                                                                                                                                      Db 24419 CACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 24460
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2000US-0216880.
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Best Local Similarity 100.
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Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; gene therapy;
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30-JUN-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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100.0%; Pred. No. 1.2e-06;
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Matches 42; Conservative
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01-SEP-2000;
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The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
                                                                                                                                                                                                                                                                         Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
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956 55 21 643 17 A0088974 A00088974 PER TOOLS 999 999 999 999 999 999 999 999 999 9	Tel: 301 838 0200 Fax: 308 838 0208 Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends. Location/Qualifiers Location/Qualifiers	Ouery Match Best Local Similarity 99.7%; Pred. No. 1.8e-44; Matches 333; Conservative 09.7%; Pred. No. 1.8e-44; Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 37 GGTCTCTACAAAATTAGCTGGATTGGGTGGGTGGCTCATGCCTATAATC 96 Db 34 GGTCTCTACAAAAATTAGCTGGGATTGGGTGGGTGGCTCATGCCTATAATC 93 QY 97 CCAGCACTTTGGGAGCTGGGTGGGTGGGTGGGTGGTTCAAGACTAGCCTATAATC 93 QY 97 CCAGCACTTTGGGAGCTGGGTGGATTGCTGAAGTTCAAGACTAGCC 153 Db 94 CCAGCACTTTGGGAGCTGGGTGGATCACTGAAGTTCAAGACTAGCC 153 Db 95 CCAGCACTTTGGGAGCTGGGTGGATCACTGAAGTTCAAGACTAGCC 153 Db 157 TGGCCAACATGGTGAAACCTTATGGAGGTGGATCACTGAAGATTGATGAAGCTAGACTAGCC 216 Db 157 TGGCCAACATGGTGAAACCTTATGGAGGTGGAGAATTGCTTGAAGCTAGAGC 216 Db 214 ACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGAAATTGCTTGAAGCTAGAGG 276 Db 214 ACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGAAATTGCTTGAAGCCTAGAGG 276 Db 214 ACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGAAATTGCTTGAAGCCTAGAGG 276 Db 214 ACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGAGCACCAGAGGGAGCCCACCAGGGGAGCCTAGGGGGAGCCCACCAGGGGAACCTGG 333 QY 337 GCAACAAGAGAAAACTGCACAAAAAAAA 370 Db 274 TGAAGGTTGTAGTGAGCCGAGATTGCACAAATGGAGGGAG	RESULT 2 T06700
2 5		S	GSS 24-MAR-199 clone 2576Pll, Euteleostomi; e; Homo. 'H., Simon, M. and r Sequence-Ready
	35 2.1 652 11 35 2.1 655 12 35 2.1 655 12 35 2.1 655 12 35 2.1 656 12 35 2.1 656 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 666 12 35 2.1 661 12 35	35 2.1 684 17 MG 35 2.1 684 17 MG 35 2.1 687 17 MG 35 2.1 687 17 MG 35 2.1 689 17 MG 35 2.1 689 17 MG 35 2.1 689 8 MG 35 2.1 689 8 MG 35 2.1 703 17 MG 35 2.1 704 10 MG 35 2.1 700 MG 30 MG	7 =

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1180 bp mRNA linear EST 02-APR-2002 5', mRNA sequence.
BQ667695.1 GI:19896741
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                                                                                /note-"Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source leukcytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 1180)

NIH-MGC http://mgc.ncl.nih.gov/.

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Ontational institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12828 row: d column: 07
High quality sequence start: 3
High quality sequence stop: 536.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 TTCTAATCAGAAACATGGAGGCCAGAAAGCAGTGGAGGAGGAGGAGGACCCTCAGGCAGCCCG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 GGAGGATGTTGTCACAGGCTGGGGCAAGGCCCTTCCGGCTACCAACTGGAGCTCTGGGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.5e-25;
0; Mismatches 1;
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/organisma"Homo sapiens"
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TITLE
JOURNAL
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603068871F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217977 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1547 row: m column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 CAAAATTAGCTGGGATTGGGTGCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGCC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TGAGGTGGGTGGATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 TACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 CCCTATCTCTACTGAAAATAYAAAAGCTAGACGTGGTGGCGCACCACCTGTAATCCCAGC
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 183; DB 14
Pred. No. 1e-25;
0; Mismatches
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/db_xref="taxon:9606"
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1. .886
                                                     Location/Qualifiers
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BI910844
BI910844.1 GI:16174292
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%;
99.3%;
                             Seq primer: M13-21
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BI910844/c
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AUTHORS
TITLE
JOURNAL
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AQ428360
CITBI-E1-2576K5.TF CITBI-E1 Homo sapiens genomic clone 2576K5, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                         GITGICACAGGCTGGGGCAAGGGCCTTCCGGCTACCAACTGGGAAGCTCTGGGAACAGCCC 703
                                                                                                                                                                                                                                                                                                              TGTTGCAAACAAGAAGCCATAGCCCGGCCAGAGCCCAGGAATGTGGGCTGGGCTGGGAGC 763
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Venter, J.C.
Use of BAC End Sequences from CalTech Libraries for Sequen Map Bulding
Unpublished (1997)
Contact: Shaying Jao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                        Length 275;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; B
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
I (bases I to 364)
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                                                                                                                                                                                                                  9.2%; Score 155; DB 12;
100.0%; Pred. No. 2.5e-20;
tve 0; Mismatches 0;
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Pred. No. 3.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCTCTGGACAGGAGTGGTCCCATCCAGGAAACC 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCICIGGACAGGAGTCCCATCCAGGAAACC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="sperm"
/note="Vector: pBeloBAC11;
CalTech Human BAC Library D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/sex="male"
               /dev_stage="Adult"
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100.08; Pic
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AQ428360.1 GI:4496126
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fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoNYs site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for [ull-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRI&t2=MRI-TN0045-120900-0095405843=2000-0912&t4=1)
Seq primer: puc 18 forward
High quality sequence srop: 4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                     944 GIGTAATCGTGTCCCTGCAAGTGTGAACAAGTGGACAAGTGTCTGGGAAGTGGAAGAGA 1003
                                                                                                                                                                                                                                                                                                                                                                                                                              1004 TCTGTGCACCATCAGGTGTGCATAGCGTCTGTGCATGTCAAGAGTGCAAGGTGAAGTG 1063
                                                                                                                                                                                                                                                                                                   884 AGTGTCAGTGTGAGTCTGTGTATGTGTGAATATTGTCTTTGTGTGGGTGATTTTCTGCRT 943
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20202663
                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 174; DB 14;
Pred. No. 1.6e-24;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone_lib="TN0045"
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                                                                                                                                                                                                         10.4%;
99.6%;
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les 224; Conservative
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FEATURES

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101 GATCACCTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCT 153
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BF746029
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//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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                                                                                                                                                                                                                                                                                                                                     B1030898 258 bp mRNA linear EST 14-JUN-2001 IL5-MT0262-290301-406-c07 MT0262 Homo sapiens cDNA, mRNA sequence.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL5&t2=IL5-MT0262-2930301-406-c07&t3=2001-03-29&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                      AAAGCTAGACGTGGTGGCACACACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAG 256
                                                            AATTGCTTGAAGCCTAGAGGTGAAGGTTGTAGTGAGCCGAGATTGCATCATTGCACAATG 316
                                                                                                                                        Gaps
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20202663
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/db_xref="taxon:9606"
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Location/qualifiers
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  Conservative
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/db_xref="taxon:0506"
/clone_llb="BT0858"
/clone_llb="BT0858"
/dev_stage="Adult"
/dev_sta
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1 (bases I to 304)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl:CM46t2:CM4-BT0858-071100-423-g016t3=2000-11-076t4=1) Seq primer: puc 18 forward High quality sequence start: 2 High quality sequence stop: 302.
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304 bp mRNA linear EST 10-JAN-200
CM4-BT0858-071100-423-g01 BT0858 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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100.0%; Pred. No. 0.26;
ive 0; Mismatches 0; Indels
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BC1-UT0033-021100-018-f12 UT0033 Homo saplens cDNA,
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Fax: +55-11-2707001
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SOURCE
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Page 12

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1..327.

(organism="Homo sapiens" / Organism="Homo sapiens" / Ab_xref="taxon:9606" / Aclone_lib=""group3" / Aclone_lib=""group3" / Aclone_lib=""group3" / Acce="organ: uterus_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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RPCII1-1706.TP RPCI-11 Homo sapiens genomic clone RPCI-11-1706, DNA
                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCI&t2=RCI-UT0033-
241100-110-fl0&t3=2000-11-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 222.
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Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Other_GSSs: RPCIII-1706.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: mdadams@tigr.org
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S.,
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Fax: +55-11-2707001
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AUTHORS
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/clone_lib="UT0033"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: pucl8; Site_l: Smal;
/note="Organ: uterus_tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-UT00333-20100-18-fl2&t3=20100-11-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 327.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 327)
1 objects. To 327)
1 bias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome
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RC1-UT0033-241100-110-f10 UT0033 Homo sapiens CDNA, mRNA sequence.
BF913166
                         Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
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100.0%; Pred. No. v..
... 0; Mismatches
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                      Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 52; Conservative
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MEDLINE
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Gaps

Linher, K.,

Euteleostomi;

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jWallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleerefedelong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end web Server:
http://www.htsc.washington.edu
Plate: 619 row: D column: 8
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACe3.6 Vector at EcoRI sites" 4 others
                                                                                                                                                                            AQ405838 13-MAR-1999 BNA linear GSS 13-MAR-1999 HS_5043_B2_B04_T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=619 Col=8 Row=D, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 519)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ309829 559 bp DNA linear GSS 22-DEC-1998
CIT-HSP-2385N1.TRB CIT-HSP Homo sapiens genomic clone 2385N1, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9789-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_Plate=619 Col-8 Row=D"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                        Score 50; DB 17; Length 519;
Pred. No. 0.55;
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Location/Qualifiers
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Conservative 0;
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AQ405838.1 GI:4415826
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AQ309829
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Homo sapiens genomic clone 2537J20,
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: bbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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/cell_type="sperm"
/notec="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
58 q 41 t
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
Class: BAC ends.
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206)
                                                                                                                                                                                                     /clone_law ...
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCILL Human Male BAC Library"
ing q 139 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 528;
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                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 17;
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.0%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 51; Conservative 0; Mismatches
                                                                                      1. .528
/organisma"Homo sapiens"
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1. .206
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                            /db_xref="GDB:7506485"
/db_xref="taxon:9606"
/clone="RPCI-11-1706"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Other_GSSs: CITBI-E1-2537J20.TR
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DNA sequence.
AQ352156
                                                                 Location/Qualifiers
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AA484228.1 GI:2213041
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Matches 49; Conserva
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AA484228
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1 (bases 1 to 584)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 29-MAY-1999
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0
                                                    Homo sapiens

Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamala; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 559)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Werter, J.C.

Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                              Email: hbe@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS_5338_B1_B05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=914 Col=9 Row=D, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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High Throughput Sequencing Center
University of Washington
VGI Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
                                                                                                                                                                                                                          Unpublished (1998)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Lekaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
713: 301 838 0200
Fax: 301 838 0208
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100.0%; Pred. No. 0.5
ilve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2385N1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT-HSP"
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AQ309829.1 GI:4041716
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Best Local Similarity 100.0
Matches 50; Conservative
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AQ563791/c
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/note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector and pBACe3.6 vector sites.
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbpp/Amage/Amage.html
Insert Length: 431 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham.
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Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones ave daribility, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ne89d07.sl NCI_CGAP_Kidl Homo sapiens cDNA clone IMAGE:911437 similar to contains Alu repetitive element; contains element MER22 AA484228
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 310)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP (1997)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"...
/clone="plate=914 Col=9 Row=D"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 584; 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 ACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 322
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Pred. No. 0.75
0; Mismatches
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/tissue_type="kidney"
/lab_host="DH10B"
                                                                                                                                                                                    http://www.htsc.washington.edu
Plate: 914 row: D column: 9
Seq primer: T7
Class: BAC ends
High quality sequence stop: 584.
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="IMAGE:911437"
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100.0%; Pre
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E Thomas and the following following the following following the following fol
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 489)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F.,

Ragal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F.,

Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Harc, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
                                                           bp DNA linear GSS 23-APR-1999
Homo sapiens genomic clone 2587123,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF771528 489 bp mRNA linear EST 12-JAN-2001
IL5-IT0027-291100-293-g02 IT0027 Homo sapiens cDNA, mKNA scquence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D" 10thers
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/db_xref~"taxon:9606"
/clone="2587123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CITBI-E1"
                                                           404
CITBI-E1-2587123.TR CITBI-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                            AQ469676.1 GI:4653330
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                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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        RESULT 18
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/note-"Vector: pAMP10; mRNA made from invasive kidney tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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llarity 100.0%; Pred. No. 1.9;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                            DB 9; Length 310; 2.2;
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                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                            Query Match 2.9%; Score 48; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 48; Conservative 0; Mismatches
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BF677661
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nes 48; Conserv
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EST 01-JUN-2000 mRNA sequence.
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CITBI-E1-2556D7.TF CITBI-E1 Homo sapiens genomic clone 2556D7, DNA
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                                                                                                                                             Site_1: EcoRI; Site_2: EcoRI; D"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessment of gene expression patterns in a model of colon tumor matastasis using a 19,200 element cDNA microarray Unpublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research
772 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                            Length 519;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAG
/note="Vector: pBluescript5Km"
a 133 c 149 g 119 t
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1.3;
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/organism="Homo sapiens"
/bratef="Leon:9606"
/clone="52461.3"
/clone=lib="CITB1-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Si
CalTech Human BAC Library D"
7 a 107 c 103 g 151 t
                                                                                                                                                                                                                                        2.9%; Score 48; DB 100.0%; Pred. No. 1.3 tive 0; Mismatches
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100.0%; Pic
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Plate: 300
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Jote_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

2 others
                                                                                                                                                 Fax: +55-11-207001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-IT0027-
291100-293-q02&t3-2000-11-29&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 447.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 519)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Muse of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Puilding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ395268 519 bp DNA linear GSS 06-MAR-1999 CITBL-E1-2546L13.TR CITBL-E1 Homo sapiens genomic clone 2546L13,
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Lidwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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  Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Chter_GSSs: CTTBT-E1-2546LI3.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
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                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IT0027"
/dev_stage="Adult"
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AQ395268
AQ395268.1 GI:4366294
                                                                                                                                     Tel: +55-11-2704922
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Best Local Similarity
Matches 48; Conserv
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20202663
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Lujyana, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

17-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japun
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:B1-45-503-9170)

Clones are dcrived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG158320 738 bp DNA linear GSS 09-JAN-2002
Pan troglodytes DNA, clone: RP43-023104.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-023104.TJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutoleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
| 159 c 169 g 186 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujjyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                              /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
a 162 c 151 g 178 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 48; DB 17; Length 735;
100.0%; Pred. No. 0.92;
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-023104.TJ"
                                                                                                                                                                                   1. .735
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-043K01.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 100.0%; Pred. No. 0.9 48; Conservative 0; Mismatches
                                                                                                                                                             Location/Qualifiers
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: EcoRI
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AG158320.1 GI:16687998
                                            Sequencing: M13Rev
                                                                                                                 : SacI
clone tracking errors.
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R.Site 2
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Matches 48; Conserva
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Clones are derived from the chimpanzee BAC library PTB This BAC end
                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 719)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       735 bp DNA linear GSS 02-NOV-2001
Pan troglodytes DNA, clone: PTB-043K01.R, genomic survey sequence.
AG057132
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                                                                                                                                                                                             Unpublished (1997)
Other_GSSs: CTTBI-E1-2556D7.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genter Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hebetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was generated during the R&D process and may have higher chance of
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Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D" 2 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Fullyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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0.94;
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100.0%; Pred. No. 0.9
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organisma"Homo sapiens"
/db_xrefa"taxon:9606"
/cloneu"2556D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CITBI-E1"
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Matches 48; Conserva
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Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balia,G.S., Simpson,D.H., Brunstein,A., deOliveire,P.S., Bucher,P., Jongeneel,C.V. O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                       Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3.UT0115-
261200-408-B08&t3=2000-12-26&t4=1)
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Seg primer: M13-21;
Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 500)
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 47; DB 17; Length 346; 100.0%; Pred. No. 3; 0; Indels
                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 CTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 238
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/organism="Homo sapiens"
/db_xref="GDB:7103832"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="2172G14"
/clone_lib="CIT-HSP"
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BF918155.1 GI:12309613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
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Zabazrovsky.E.R. Gizatullin, R., Podowski,R.M., Zabarovska,V.V., Xie
L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J.,
Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
NotI clones in the analysis of the human genome
Nucleic Acids Res. 28 (7), 1635-1639 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Lung; DNA was isolated from A549 cells after sodium arsenite exposure for 4 weeks. This fragment was differentially methylated relative to untreated controls and was identified using methylation sensitive AP-PCR and
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1 (bases 1 to 340).
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 Length 738;
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                                                                                                              220 CCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
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            DB 17;
0.91;
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/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
      2.9%; ...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
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Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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100.0%; Pre
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                                                      Conservative
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          Query Match
Best Local Similarity
Matches 48; Conserv
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Gaps

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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 989)
Zabarovsky, E. R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V., Xie, L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N., Li, J., Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and Wahlestcdt, C. Noti clones in the analysis of the human genome
Noti clones Acids Res. 28 (7), 1635-1639 (2000)
                                                                                                                                                                                                                                                 AQ937652 BAB bp DNA linear GSS 23-AUG-2000 NB6-242C Human NotI clones Homo sapiens genomic, DNA sequence. AQ937652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note:"Organ: Lung; DNA was isolated from A549 cells after sodium arsenite exposure for 4 weeks. This fragment was differentially methylated relative to untreated controls and was identified using methylation sensitive AP-PCR and
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Eukaryota: Eutheria: Primates: Catarrhini: Hominidae: Homo.
(Dases 1 to 122)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapolli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
                                                   Gaps
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  2.8%; Score 47; DB 17; Length 658; 100.0%; Pred. No. 1.6;
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Pred. No. 1;
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                                              0; Indels
                                                                                                                356 CACCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTT 310
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/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
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100.0%; Pred. No. 1,
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                  100.0%; Pred. No. 1.0
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Email: Raf.Podcwski@cgr.ki.se
Class: NotI slite.
Location/Qualifiers
1. 989
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Center for Genomics Research
Karolinska Institute
1177 Stockholm, Sweden
Tel: +46-8-728-6372
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                                            47; Conservative
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                       Best Local Similarity
Matches 47; Conserv
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                                                                               /organisme"Homo sapiens"
/db_xrefr"taxon:9606"
/db_xrefr"taxon:9606"
/dclone_lib="UT0115"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG099522.1 GI:16720039 GSS. Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-101N05.R. Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-Aug-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpesegesc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpenace BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 03-NOV-2001
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Pan troglodytes DNA, clone: PTB-101N05.R, genomic survey sequence.
AG099522
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. A. Sequences of Library PTB Unpublished

2 (bases 1 to 658)
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201 c 122 g 204 t 2 others
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/db_xref="taxon:9598"
/clone=="PTB-101N05.R"
                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 47; DB 100.0%; Pred. No. 2.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                              low stringency conditions.
124 c 124 g 149
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                     High quality sequence stop: 465.
Location/Qualifiers
1. .500
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primer: puc 18 forward
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R.Site 1 : SacI
R.Site 2 : SacI.
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Matches 47; Conservative
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,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opinity NCI_CGAP_Kid6 bp mRNA linear EST 13-APR-1999 opinits to contains Alu repetitive element; contains L1.t3 L1 AA971049 AA971049.1 GI:3146339
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                      High qality sequence stops: 90 Source: IMAGE Consortium, LLNL This colone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 467 Std Error: 0.00
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:71538"
/clone_lib="Stratagene fetal spleen (#937205)"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="9ClR cells (kanamycin resistant)"
/note="0rgan: spleen; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: KhoI; Cloned unidirectionally.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                         Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
Emall: est@watson.wustl.edu
Insert Size: 467
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Email: gappbs-refmail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 122;
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/organism="Homo sapiens"
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Best Local Similarity 100.0
watches 46; Conservative
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Unpublished (1997)
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/tissue_type="kidney tumor"
/lab_host="SoLR (kanamycin resistant)"
/lab_host="Organ: kidney; Vector: Bluescript SR-; Site_1:
EcoRI; Site_2: Xhol; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors, 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGACTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPCI-11-230012.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-230012.
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Primates; Catarrhini; Hominidae; Homo.
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Other_GSSs: RPCI-11-230012.TV
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Clones are derived from the human BAC library RPCI-11. For BAC
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
found through the I.M.A.G.E. Consortium/LLNL at:
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                          www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1387 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 325.
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100.0%; Pred. No. 4.3;
live 0; Mismatches
                                                                                                                                                              1. .368 // Accordantsm="Homo sapiens" / Organism="Homo sapiens" / Ab_xref="texon:9606" / Clone="InhaRE:1575313" / Clone="Inha" NCI_CGAP_Kid6" / Sex="mixed"
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/db_xref="GDB:7588283"
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/clone="RPC1-11-230012"
/clone_lib="RPC1-11"
/sex="Male"
                                                                                                                                            Location/Qualifiers
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Mammalia; Eutheria;
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AG175442/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 509)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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$3244_BL_D05_T7 CIT Approved Human Genomic Sperm Library D Homo

$40216073

$60216073 I GI:3631393

$60216073.1 GI:3631393
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones in
                   EcoRI; Site_2: EcoRI;
                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 46; DB 17; Length 509; ilarity 100.0%; Pred. No. 3.1; Conservative 0; Mismatches 0; Indels
                                                                                                    Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                   4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 others
                                                                                                                                                                                       174 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATCT 219
                                                                                                                                                                  136 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATCT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 CTATAATCCCAGCACTTTGGGAGCCTGAGGTGGGTGGATCACCTGA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 CTATAATCCCAGCACTTTGGGAGCCTGAGGTGGGTGGATCACCTGA 134
                                                                                                                                     0;
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
FPCIII Human Male BAC Library"
1 102 c 113 f 9 113 t
                                                                                                  DB 17;
3.2;
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                                                                                                  2.7%; Score 46; DB 100.0%; Pred. No. 3.2 Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone:"Plate=3244 Col=9/clone_lib="CIT Approved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (206) 616-3618
Fax: (206) 616-3887
Email: juallace@u washington.edu
Sequence Tagged Connector
Plate: 3244 row: H column: 9
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 509.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex~"male"
                                                                                                                                     46; Conservative
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Matches 46; Conserva
                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                    Query Match
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                                                                                                                                                                                                                                                    RESULT 33
AQ216073/c
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ORGANISM
                                                BASE COUNT
ORIGIN
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.mecl.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seg primer: 77
                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 3 others
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Pan troglodytes DNA, clone: RP43-046G04.T7, genomic survey
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Male BAC Library clone:RP43-046G04.T7.
Pan troglodytes
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Pan.
                                                                                                                                     Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelc
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
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/clone_lib:"RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATCT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"/db_xref="taxon:9606"
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Location/Qualifiers
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AG175442.1 GI:16705122
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Local Similarity
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ORIGIN
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AW265384/c
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TITLE
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                Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Ranagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.ip, URL:http://hgp.gsc.riken.go.ip/,
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xg35d09.x1 NCI_CGAP_Ut1 Homo sapiens CDNA clone IMAGE:2629553 3/
similar to contains Alu repetitive element;, mRNA sequence.
AW150028.1 GI:6197934
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 306.
Location/Qualifiers
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

No. Coap http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
226 c 157 g 245 t 3 others
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2;
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1. 789
/organism="Pan troglodytes"
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/clone_lib="NCI_CGAP_Ut1"
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/clone="RP43-046G04.T7"
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/db_xref="taxon:9606"
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: EcoRI
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      (bases 1 to 789)
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                            Vector
R.Site 1
R.Site 2
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AW150028/c
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                    AUTHORS
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Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Non-directionally cloned into the UDG sites of pAMPl0.
Size-selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
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                                                                       /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2754212"
/clone_lib="NOT_CGAP_HN7"
/tissue_type="normal squamous epithelium, floor of mouth"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAILONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AW265384.1 GI:6642200
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0
//tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                 DB 10; Length 403; 6.1;
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6;
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100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pred. No. v.
'.. 0; Mismatches
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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/Organism: view organism: / Organism: view organism organism
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298 bp mRNA linear EST 11-JUN-2001
4 Homo Sapiens cDNA clone ax44d12 random, mRNA sequence.
BG943962
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40mi3 fwd. ET from Amersham
High quality sequence stop: 241.
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Fax: 301 435 5148
Email: jm/f@nih.gov
DNA Sequencing and analyses by National Institutes of Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 298)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
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Pred. No. 13;
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Plate: 44 row: d column: 12
Seq primer: -21M13 forward primer (ABI).
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/organism∾"Homo sapiens"
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/organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone="ax44d12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG943962.1 GI:14343334
Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 262)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                AQ105410 262 bp DNA linear GSS 28-AUG-1998 HS_2003_B1_G01_MR CIT Approved Human Genomic Sperm Library D Homo saptens genomic clone Plate=3023 Col=1 Row=N, DNA sequence. AQ105410
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1 (bases 1 to 281)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Molte,Y., Wylls, Stellenberg,K., Steptoe,M., Tan,F., Theising,B., WashU-NCI human EST Project
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/db_xref="taxon:9606"
/clone="piate=30:30 Col=1 Row=N"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Val Queen Anne Avenue North, Seattle, WA 98109, USP
Tel: (206) 616-3887
Eax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3023 row: N column: 1
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Location/Qualifiers
1. .262
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AA630672/c
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                                                      RESULT 38
                                                                                                                                                                                                          ACCESSION
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Best Local Similarity
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BG006754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                           /note="Organ: blood; Vector: Lambda ZAP II; Site 1: ECORI; Site 2: ECORI; 65,000 proliferating erythroid cells from the buify coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoletin. Total RNA was purified from the sorted cell population using TRIZOL reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's Cappinder CDNA Library Construction Rit (Clontech) according to the manufacturer's protocol and cloned into ECORI digested Lambda Zap II vector (Strategene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the CDNA inserts were sequenced in high http://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 341)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI031739 341 bp mRNA linear EST 14-JUN-2001
ILS-MI0266-100401-410-h08 MI0266 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-MT0266-
100401-410-h08&t3=2001-04-10&t4=1)
/clone_lib="Proliferating Human Erythroid Cells (LCB:ax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                    /cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Score 44; DB 13; Length 298; 100.0%; Pred. No. 13; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATCTCTA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 GAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCCTATCTCTA 207
                                                                     /tissue_type="blood"
/cell_type="Erythroid Cells"
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Location/Qualifiers
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                                                                                                                                                                                               /lab_host="SOLR"
                                                      /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI031739.1 GI:14438369
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Les 44; Conservative
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BI031739
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VERSION
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/db_xref="taxon:0606"
/clone_lib="MT0266"
/dev_stage="Adult"
/note="Organ: marrow: Vector: pucl8; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES FOR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., ds Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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//dev_stage="Adult"
//note="Organ: placenta_normal; Vector: puc18; Site_1: Smal
// Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-GN0194-
271100-023-C11&t3=2000-11-27&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 345.
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mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \operatorname{Simpson}, A . J. Shotgun sequencing of the human transcriptome with ORF expressed
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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0
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20202663
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 341;
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%; Score 44; DB
100.0%; Pred. No. 11;
iive 0; Mismatches
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="GN0194"
                                                                                                                                                                                                                                                                                                          stringency conditions."
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Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                                                                    88 9
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BG006754.1 GI:12450255
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Conservative
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AG158858 673 bp DNA linear GSS 09-JAN-2002
Pan troglodytes DNA, clone: RP43-024D09.TJ, genomic survey
                                                            AQ415807 APCI-11 Homo sapiens genomic clone RPCI-11-207K20.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please context belong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee BAC Library clone:RP43-024D09.TJ.
                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                          for Sequence-Ready
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
103 c 96 g 173 t
                                                                                                                                                                                                                                                                                                                              Primates; Catarrhini; Hominidae; Homo.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of BAC End Sequences from Library RPCI-11 for Sequence building
Map Building
Unpublished (1997)
Other Cass: RPCI-11-207K20.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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100.0%; Pred. No. 7.8;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 TAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA
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/db_xrefe"GDB:7579363"
/db_xrefc"taxon:9606"
/clonec"RPCI-11-207K20"
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Eukaryota; Metazoa;
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Eukaryota; Metazoa;
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                                                                                                                     DNA sequence.
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Best Local Similarity
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/db_xref="taxon.9606"
/clone_lib="ET0174"
/dev_staige="Adult"
/dev_staige="Adult"
/note="Organ: lung_tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal, A min1.library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (bases 1 to 41%)
1 (bases 1 to 41%)
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1 (bases 2 to 41%)
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=QV3&t2=QV3-ET0174-
291100-506-905&43%-2000-11-29&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 469.
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mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                    Length 345;
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                                                                                 Ouery Match 2.6%; Score 44; DB Best Local Similarity 100.0%; Pred. No. 11; Matches 44; Conservative 0; Mismatches
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llarity 100.0%; Pred. No. 7.9
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BF880329.1 GI:12270455
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Fax: +55-11-2707001
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/db_xref="taxon:9606"
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Best Local Similarity 100.9
Matches 43; Conservative
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                                Chases I to 673)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Direct Submission
Submitted (12-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Conter (6SC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC Library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 113.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB78490

185 bp mRNA linear EST 25-MAR-199
est5b09.21 NCI_CGAP_0v2 Homo saptiens cDNA clone IMAGE:1385445
similar to contains Alu repetitive element; contains element MER22
repetitive element; mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 185)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Bmall: gapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael
Emmert-Buck, M.D., Ph.D.
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1 others
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5.6;
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/clone_lib="RPCI-43 Chimpanzee
118 c 154 g 201 t
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BAC end sequences of Library RPCI-43
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/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9598"
/clone="RP43-024D09.TJ"
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                                                                                                                                                                                                                                                                                               Sequencing: TJ
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Matches 44; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:966"
/clone_lib="GN0349"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                              /tissue_type="ovary"
/lab_host="DHIOB"
/note="vector: paMPI0; mRNA made from invasive ovarian
tumor, cDNA made by oligo-dr priming. Non-directionally
cloned. Size-selected on agarose gel, average insert size
600 bp. Reference: Krizman et al. (1996) Cancer Research
56:5380-5383.
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0
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matskuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 15-JUN-2001
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-GN0349-300101-002-c05&t3=2001-01-30&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      одужения 18-7UN-200 MRNA linear EST 15-JUN-200 MR3-GN0349-300101-002-c05 GN0349 Homo sapiens cDNA, mRNA sequence. BI054067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%; Score 43; DB 9; Length 185; 100.0%; Pred. No. 31; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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/clone="IMAGE:1385945"
/clone_lib="NCI_CGAP_Ov2"
/sex="female"
                                                                                                                                                                                                                                                                                                                        42 g
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ò a

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/Organism."Homo sapiens"

/db_xrefr"taxon:9606"

/dbox1612"

/dev_stage="Adult"

/note="Organ: testis_normal; Vector: puc18; Site_1: Smal;

Site_2: Smal; A min1-library was made by cloning products
derlived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                           Eukaryotz, Metazoa; Chordata; Craniata; Vertcbrata; Eutelcostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 392)

1 (bases I to 392)

Dias Neto, E., Garcia Correa, R., Verjovski-Almelda, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carralho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongencel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Rels, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 17-MAY-2000 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl:mR4&t2:MR4-TN0112-171100-206-a09&t3-2000-11-17&t4-1)
Seq primer: puc 18 forward
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MR4-TN0112-171100-206-a09 TN0112 Homo sapiens cDNA, mRNA scquence.
BF888753
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto,E., Garcia Correa,R., Verjovski-Almelda,S., Briones,1
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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20202663
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QV4-ST0233-251199-041-a10 ST0233 Homo sapiens CDNA,
AW816343
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107 g 90 t
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llarity 100.0%; Pred. No. 15;
Conservative 0; Mismatches
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High quality sequence stop: 392.
Location/Qualifiers
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                                                            BF888753.1 GI:12279999
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                                                                                                                                                     Homo sapiens
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Best Local Similarity
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                                                                                                                           human.
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                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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/organism="Homo sapiens"
/db_xref="Choroling"
/db_xref="taxon:960s"
/db_xref="taxon:960s"
/clone="IMAGE:397491"
/clone="IMAGE:397491"
/clone="IMAGE:397491"
/clone="Image:397491"
/clone="Image:397491"
/clone="Image:397491"
/lab_host="BullOB (ampicillin resistant)"
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I; Site_2: Eco RI;
ist stranded cDNA was size selected, Iliqated to Eco
RI adapters (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of a modified pT73 vector
//beach.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 314)
Hiller.L. Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marta,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
Washle,Y., Wylle,T., Waterston,R. and Wilson,R.
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                         AA701080
314 bp mRNA linear EST 19-DEC-1995 2957h02.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397491 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Ef from Amersham
High quality sequence stop: 301.
Location/Qualifiers
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                            Length 185
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                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 TAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGA 128
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                                                            DB 13;
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                                                         2.6%; Score 43; DB
100.0%; Pred. No. 31;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.6%; Score 43; DB Best Local Similarity 100.0%; Pred. No. 18; Matches 43; Conservative 0; Mismatches
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85 c 66 g
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AA701080.1 GI:2704245
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Eukaryota; Metazoa;
Mammalia; Euthería;
                                                                                     Best Local Similarity 100.
Matches 43; Conservative
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1. .430
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/clone_lib="S70233"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                      Fel: +55-11-2704922
Fax: +55-11-2707001
Bmall: asimpson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-ST0233-251
199-041-a10&t3=1999-11-25&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 430.
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Fua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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2.6%; Score 43; DB 10; Length 430;
Best Local Similarity 100.0%; Pred. No. 13;
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CORRESPONDENCE ADDRESS:
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Sequence 13,
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TITLE OF INVENTION: P450DB1 CLONES FOR IDENTIFYING HUMANS; WITH GENETIC DEFECT IN DRUG METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 3.6%; Score 61; DB 6; Le
Similarity 100.0%; Pred. No. 1.2e-16;
61; Conservative 0; Mismatches 0;
PCT-US95-10202-20
PCT-US95-10203-20
BCT-US95-10220-20
BC-09-38-20-20
BC-09-38-20-4-13
BC-09-38-630-4
BC-09-38-630-5
BC-07-914-281-5
BC-07-914-281-5
BC-08-656-731-5
BC-08-656-731-5
BC-08-656-731-5
BC-08-611-587-1
BC-08-167-681-45
BC-08-167-681-4
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US-09-078-294-7
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,158
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 845,507
FILING DATE: 27-FEB-1992
APPLICATION NUMBER: 292,815
FILING DATE: 03-JAN-1989
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Patent No. 588174
GENERAL INFORMATION:
APPLICANT: Wolf, Charles R.
APPLICANT: Spurr, Nigel K.
APPLICANT: Gough, Alan C.
TITLE OF INVENTION: GENETIC ASSAY
NUMBER OF SEQUENCES: 25
      6769
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1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCCATCTTCCTGCTCCTGGTG 1679
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SHAPIRO, MORIN & OSHINSKY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP 2101 L Street N.W.
                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/145,658D
FILING DATE: 04-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9001181.8
FILING DATE: 18-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/732,223
FILING DATE: 18-JUL-1991
ATTONNEY, AGGNT INFORMATION:
NAME: Brady, Jr., James W.
REFERENCE/DOCKET NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Fatent No. 5981174
GENERAL INFORMATION:
APPLICANT: Wolf, Charles R.
APPLICANT: Miles, John S.
APPLICANT: Spurr, Nigel K.
APPLICANT: Gough, Alan C.
TITLE OF INVENTION: GENETIC ASSAY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORMATION FOR LEGISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 1566 base pairs TYPE: nucleic acid CTRANDEDNESS: single
             2101 L Street
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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DICKSTEIN,
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                       Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
US-08-145-658D-13
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US-08-145-658D-22
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1620 ATGGGGCTAGAAGCACTGGTGCCCCTGGCCGTGATAGTGGCCATCTTCCTGCTCCTGGTG 1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP STREET: 2101 L Street N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,658D
FILING DATE: 04-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                       FILING DATE: 18-JUL-1991
ATORNEY/AGENT INFORMATION:
NAME: BREGY, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.017
TELECHONE: 202-785-9700
TELEPHONE: 202-887-0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08145658D
Patent No. 5981174
GENERAL INFORMATION:
APPLICANT: Wolf, Charles R.
APPLICANT: Miles, John S.
APPLICANT: Spurr, Nigel K.
APPLICANT: Gough, Alan C.
TITLE OF INVENTION: GENETIC ASSAY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                        FILING DATE: 18-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/732,223
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APPLICATION NUMBER: US 07/732,223
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9001181.8
FILING DATE: 18-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-887-0689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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MOLECULE TYPE: C
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,658D
FILING DATE: US/08/181.8
FILING DATE: US/08/181.8
FILING DATE: US/08/181
ATPOREX/ACENT INFORMATION:
NAME: BTADY, Jr., James W.
REGISTRATION NUMBER: 32,115
FELEPHONE: 202-785-9700
FELEFRAX: 202-887-0689
INFORMATION FOR SEC ID NO: 22:
ELECOMMUNICATION INFORMATION:
TELEFRAX: 202-887-0689
INFORMATION FOR SEC ID NO: 22:
ELECOMMUNICATION INFORMATION:
TELEFRAX: 202-887-0689
INFORMATION FOR SEC ID NO: 22:
ELECOMMUNICATION INFORMATICS:
LEWCTH: 1566 base pairs
TYPE: NUCLEIC acid
STANDEDERSS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/145,658D
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Patent No. 5981174
GENERAL INFORMATION:
APPLICANT: Wolf, Charles R.
APPLICANT: Spurr, Nigel K.
APPLICANT: Gough, Alan C.
TITLE OF INVENTION: GENETIC ASSAY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DICKSTEIN, SHAPIRO, MOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2101 L Street N.W. CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: GDP-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANGFERAGES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
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Patent No. 6235879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hayden. Michael R.
APPLICANT: Huq, A.H.M. Mahbubul
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Chopra, Vikramjit Singh
TITLE OF INVENTION: Michael
TITLE OF INVENTION: Huntington's Disease Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                   E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1316 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCC 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAAACCC 176
                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
2.4%; Score 41; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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PO Box 5270
                            ROUQUIER, SYLVIE
GIORGI, DOMINIQUE
KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEEX: 248855 OPAT UR
INFORMATION FOR SCO ID NO: 7:
SEQUENCE CHARACTERISTICS:
         GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2115 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                    VIRGINIA
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STREET: FO
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STREET: 17
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US-09-085-199B-44
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US-08-395-800A-7
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                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                APPLICANT
                                                                                                                                                                                                                                                                                                  STATE:
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APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION:
ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION:
NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION:
UNCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF LINCHART OF THE REFERENCE:
CURRENT FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEO, ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 42; Conservative 0; Mismatches 0;
                                          NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08395800A
Patent No. 5807732
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LCCATION: (1)...(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09797906 Patent No. 6329188
                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 202-785-9700
                                                                                                                                                 TELEFAX: 202-887-0689
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1571 base pairs
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.6 Best Local Similarity 100. Matches 61; Conservative
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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US-08-145-658D-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 84495
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US-08-395-800A-7
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US-09-797-906-3
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GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
APPLICANT: SIGNATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: ISCLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
IMMUNOGLOBULIN E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 38; DB 1; Length 11298; 100.0%; Pred. No. 3.9e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
ATHORDROW. A. C. ASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6813 CAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 6850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-920A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
APPLICANT: AJOUVIN, MALÍE-Helene
TITLE OF INVENTION: ISOLATION, CHARACTERIZA,
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF
TITLE OF INVENTION: IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                   Suite 500
                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08201879A
; Patent No. 5807988
                                                                                                                                                                       SSEE: Foley & Lardner
F: 1800 Diagonal Road,
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703)663-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 11298 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCRI beta
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lin
ORIGINAL SOURCE:
                                                                                                                                                                              ADDRESSEE:
STREET: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; STRAIN:
US-07-869-933-31
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US-08-201-879A-2
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                                                                                                                                                                                                                                                 STATE:
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Sequence 3. Application US/09754250

Sequence 3. Septication US/09754250

GENERAL INFORMATION:

APPLICART: WEL, MING-HUI et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PHOSPHODIESTERASE

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001063

CURRENT APPLICATION NUMBER: US/09/754,250

CURRENT FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 111282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: exon 29 and partial cds of HIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1839 TCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 3879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 TCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
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                                                                                                                                                                                                   UBC.P-013US2
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-07-869-933-31
; Sequence 31, Application US/07869933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(111282)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32.38
REFERENCE/DOCKET NUMBER: UBC.
TELECOMMUNICATION INFORMATION:
TELEFANO: (970) 668-2050
TELEFAN: (970) 668-2052
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
OPERATING SYSTEM: MS DOS 5.0 SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                     SEQUENCE.
LENGTH: 3715
LENGTH: 3715
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-085-199B-44
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Gaps

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USA
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                  LENGTH: 112132
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                                               US-09-741-150-3/c
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US-08-257-963B-10
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Patent No. 6111803
GENERAL INFORMATION:
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta TITLE OF INVENTION: subunit of the high affinity receptor for TITLE OF INVENTION: jamunoglobulin E.
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT APPLICATION NUMBER: 07/869,933
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEO ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: join(456..511, 1381..1510, 2026..2160, 4475..4531, LOCATION: 5079..5237, 5640..5738, 7224..7319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 11298; 3.9e-07;
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 CAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
                                                   FILING DATE: 24 FEB 1994
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 07/869,933
FILING DATE: 16-APR-1992
PRIOR APPLICATION NUMBER: US 07/859,03419
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BERT, STEPHEN 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Score 38; DB 100.0%; Pred. No. 3.9 Live 0; Mismatches
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                                    UMBER: US/08/201,879A
24-FEB-1994
                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11298 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-103-663-31
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ORGANISM: Homo sa
STRAIN: FCRI beta
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Matches 38; Conserv
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LENGTH: 11298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CILE REPERENCE: CL000968
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT APPLICATION NUMBER: US/09/741,150
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia: Schwartz, Joan P.;
APPLICANT: Patricia: Patricia: APPLICANT: Patricia: APPLICANT: APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match 2.3%; Score 38; DB 4; L. Eest Local Similarity 100.0%; Pred. No. 3.2e-07; Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GTGGTGGCACACCTGTAATCCCAGCTACTTAGGAGG 244
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APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 346.34
REFERENCE/DOCKET NUMBER: 20064126US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/257,963B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 10, Application US/08257963B
; Patent No. 5840686
; Sequence 3, Application US/09741150 ; Patent No. 6436689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; DCGATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
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TELEFAX: (
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Gaps
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APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Tanivaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                    7.0 kb No. 6319687 1-No. 6319687 fragment; Derived from human placental genomic DNA; also referred to as JT106
                                                                                                                                                                                                                                                                                                                                                                                           Length 7210;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%; Score 37; DB 4; Length 721 Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 37; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-UNN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-UNN-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-UNN-1994
PROFINEY/AGENT INFORMATION:
NAME: DOROTHY R: AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 320264126PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
PCT-US95-07201-10
; Sequence 10, Application PC/TUS9507201
; GENERAL INFORMATION:
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TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                   MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                   LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION: Frac
OTHER INFORMATION: Frac
            Double
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                                    Unknown
                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: DASH II
                                                                                                       ORGANISM: Human
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New York
                                                                                                                                                                                                    NAME/KEY: JT6A
            STRANDEDNESS:
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ZIP: 10154
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STATE:
                                                                                                                                                                         FEATURE:
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Sequence 10. Application US/08367841A
Betch No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Garald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tihk, Joyce
TITLE OF INVENTION: PIGMENT EPTTHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: OGGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                            COCATION:
COCATION:
COCATION:
COTHER INFORMATION: 7.2 kb No. 5840686 1 fragments
COTHER INFORMATION: Derived from human placental genomic DNA
US-08-257-9638-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%; Score 37; DB 2; Length 7210; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 37; Conservative 0; Mismatches 0; Indels
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REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMUNICATION INFORMATION:
TELEFRAX: (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION 35
FROM APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 08/257,963
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morgan & Finnegan
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLEOLLE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 345 Park Avenue
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                            LIBRARY: DASH II
                                                                                                                                                                                                                                                                                           NAME/KEY: JT106
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Tombran-Tink, Joyce
Typerion: PIGMENT EPITHELIUM
FENTION: DERIVEDE FACTOR: CHARACTERIZATION GENOMIC
FENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF plus flanking sequences.
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APPLICANT: Particla; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2%; Score 37; DB 4; Length 22481;
100.0%; Pred. No. 9.6e-07;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3057 GCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 3093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 GCGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
      Chader, Gerald J.; Rodriguez, Ignacio R.; Mazuruk, Krzysztof;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20264126US2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/367,841A FILLING DATE: 30-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULGASIELCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                          NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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IDENTIFICATION METHOD:
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                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 37; Conserve
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                                                                                                                                                                                                                                                                                                 New York
New York
                                                                                                                                                                                                                                                                                                                                                           USA
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PCI-US95-07201-43
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US-08-367-841A-43
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                  APPLICANT:
                                    APPLICANT:
                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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| Steele, Finten R |
| APPLICANT: Steele, Finten R |
| APPLICANT: Steele, Finten R |
| APPLICANT: Chader, Gerald J |
| APPLICANT: Chader, Gerald J |
| APPLICANT: Chader, Gerald J |
| APPLICANT: Decrara, Sofia P |
| APPLICANT: Denson, Lincoln V |
| APPLICANT: Rodriguez, Ignacio R |
| TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR |
| FILE REFERENCE: 2026-4203051 |
| CURRENT APPLICATION NUMBER: 08/29, 979 |
| FRIOR PILING DATE: 1995-01-25 |
| PRIOR FILING DATE: 1995-06-04 |
| PRIOR FILING DATE: 1992-06-04 |
| PRIOR FILING DATE: 1992-09-24 |
| NUMBER OF SEQ ID NOS: 34 |
| SEQ ID NO 4 |
| SEQ ID NO 4 |
| SED ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                   fragment; Derived from human placental genomic DNA; also referred to as JT106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
. 1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 37; DB
100.0%; Pred. No. 1e-
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2%; Score 37; DB 100.0%; Pred. No. 9.9
                                                                                                                                                                                                                                                                                        7.0 kb Not 1-Not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08520373D Patent No. 6451763
                              Genomic DNA
                                                                                                                                                                                                                        LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION: 7.0
OTHER INFORMATION: frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.2%
Best Local Similarity 100.0
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
Unknown
                                                                                                                                            LIBRARY: DASH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 37; Conserv
                                                                                  Human
                                                                                                                                                                                                  NAME/KEY: JT6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                        MOLECULE TYPE: (ORIGINAL SOURCE:
                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-07201-10
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                                                                                  ORGANISM:
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100.0%; Pred. No. 8.7e-07;
ive 0; Mismatches 0; Indels
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US-09-078-204-3/C
Sequence 3. Application US/09078294
Sequence 6. 2626211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT APPLICATION NOWER: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
TILE AND CANCILLA, Michael R.
FILE REFERENCE: Davies Col
FURENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                         3057 GCGCTCGTCCTATAATCCCAGCACTTTGGGAG 3093
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100.0%; Pred. No. ...
0; Mismatches
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US-09-078-294-3
                                                                                                                                                                  LOCATION: 1...22484
COTHER INFORMATION: "n" means either a, c, US-09-875-223-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09078294; Patent No. 6265211; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 37; Conservative
    NUMBER OF SEQ ID NOS: 2
SOFWHARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 22484
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Best Local Similarity 100.0
Matches 37; Conservative
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Best Local Similarity 100.
Matches 37; Conservative
                                                                                                      ORGANISM: Homo sapiens
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LENGTH: 80246
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LENGTH: 80595
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CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: No. 6391850thwestern University
APPLICANT: No. 63918501 Bouck
APPLICANT: David Dawson
APPLICANT: Paul Gillis
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
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Patent No. 6391850
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Nucleic Acid
DEDNESS: Double
OGY: Unknown
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MOLECULE TYPE: Genomic DNA
: 345 Park Avenue
New York
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Best Local Similarity 100.0
Matches 37; Conservative
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CON: 90819..90865
INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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INFORMATION: complement polymorphic fragment 99-1437-325
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INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261
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NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273
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INFORMATION: polymorphic fragment 5-124-273
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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment
              5-135-198
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LOCATION: 97099..97145
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FEATURE:
ION: 108149
INFORMATION:
                                                        LOCATION: 108308
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 146345
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OTHER INFORMATION:
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LOCATION: 72771..
OTHER INFORMATION
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NAME/KEY: allele
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LOCATION: 150329
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LOCATION: 160031
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LOCATION: 90819.
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BOUGUELER, Lydie
APPLICANT: BOUGUELER, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.0314
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
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OTHER INFORMATION: 5-135-155 : polymorphic base insertion FERJUME:
NAME/KEY: allele
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        113 CTGAGGTGGGTGGATCACCTGAAGTCAGGAGTTCAAG 149
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                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                          Sequence 1, Application US/09345882 Patent No. 6399373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION: 90842
INFORMATION: 99-1437-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99-1442-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 5-127-261
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OTHER INFORMATION: 5-130-257
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                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION
FEATURE:
NAME/KEY: allele
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LOCATION: 72794
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LOCATION: 88073
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NAME/KEY: allele
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LOCATION: 99117
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NAME/KEY: allele
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LOCATION: 103806
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                                                                                           US-09-345-882-1/c
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Gaps
                                                            GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION UNMBER: US/09/128,155
CURRENT FILING DATE: 1998-07-02
EARLIER PILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: FEALES OF CANINGWAS VERSION 3.0
SEQ ID NO 16
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US-09-426-290-1/C
Sequence 1, Application US/09426290
Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gilcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
                    ; Sequence 16, Application US/09128155
; Patent No. 6117654
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; OTHER INFORMATION: n - A,T,C or G
US-09-128-155-16
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; LOCATION: (128910)...(129139)
US-09-426-290-1
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LOCATION: (21181)...(21403)
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ORGANISM: Homo Sapiens
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US-09-128-155-16
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NAME/KEY:
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                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: allole
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID55
FEATURE:
NAME/KEY: allele
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                          ID71
                                                                                                          FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
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LOCATION: 103783..103828
OTHER INFORMATION: POlymorphic fragment 5-131-395 SEQ ID36
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NAME/KE:
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
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OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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                                       NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ
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Best Local Similarity 100.(
Matches 37; Conservative
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LOCATION: 106918..106966
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LOCATION: 108084..108130
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NAME/KEY: allele
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LOCATION: 103783.
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FEATURE:

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Length 168575;

Query Match 2.1%; Score 36; DB 4; Le Best Local Similarity 100.0%; Pred. No. 2.2e-06; Matches 36; Conservative 0; Mismatches 0;

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GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0904
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT FILING DATE: 2000-12-06
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APPLICANT: LI, Jiayin et al
TITLE OF INVENTION: ACID HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MALECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: 2000831
CURRENT APPLICATION NUMBER: US/09/735,934A
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
           TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLETC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000849
CURRENT APPLICATION NUMBER: US/09/738,884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SSOFTWARE: FASLEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 13953
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6.9e-06;
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6.5e-06;
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100.0%; Pred. No. c
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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; Patent No. 6426206
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Best Local Similarity 100.
Matches 35; Conservative
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Best Local Similarity 100.(
Matches 35; Conservative
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                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-738-884-3
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US-09-729-995-3
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US-09-735-934A-3
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US-09-729-995-3
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                                                                                                       RESULT 26
US-09-305-384-5
; Sequence 5, Application US/09305384
; Patent No. 624218
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.;
APPLICANT: Heartlein, Michael W.;
APPLICANT: Selden, Richard F.;
TITLE OF INVENTION: SEDWOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/01701
; CURRENT APPLICATION NUMBER: US/09/305,384
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,649
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 624218
Patent No. 624218
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richael W.
TITLE OF INVEWTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY FILE REFERENCE: 07236/017001
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER FILING DATE: 1998-05-05
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SCETTARE: FastSEQ for Windows Version 3.0
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7.3e-06;
0;
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159 AGACTAGCCTGGCCAACATGGTGAAACCCTATCTC 193
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Patent No. 6391606
SEMERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.19
Best Local Similarity 100.(
Matches 35; Conservative
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; ORGANISM: Homo sapiens
US-09-305-384-5
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US-09-305-384-1
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                               OTHER INFORMATION: 20-841-149 : polymorphic base A or G
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CCATION: 15222.15240
CTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242.15260
COTHER INFORMATION: 17-41-250.mis
COCATION: 15242.15260
CTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
CTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42337
CTHER INFORMATION: 20-841-149.mis complement
LOCATION: 42219..42337
CTHER INFORMATION: 20-841-149.mis complement
LOCATION: 42429..45441
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OTHER INFORMATION: 17-42-319.mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 12348. 12366
OTHER INFORMATION: 17-42-319.mis complement
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COCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 45328..4584
COCATION: 45328..4584
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45863
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 75644..7664
COCATION: 77166..77185
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77186
OTHER INFORMATION: 20-853.rp
COCATION: 1220..1238
OTHER INFORMATION: 20-863.rp
NAME/KEY: primer_bind
LOCATION: 1220..1238
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 20-828.rp complement AMBE/KEY: primer_Dind LOCATION: 12029..12050 OTHER INFORMATION: 17-42.pu
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OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443.45461
                                                                                                                                  NAME/KEY: allele
LOCATION: 77058
COTHER INFORMATION: 20-853-415:
NAME/KEY: Primer_bind
LOCATION: 229.949
OTHER INFORMATION: 20-828.pu
                                                                                                              OTHER INFORMATION: 20-842-115
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LOCATION: 1357..1377
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                                                     NAME/KEY: allele
LOCATION: 45442
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APPLICANT: Benison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bour, Barbara
APPLICANT: Bithain, Bernard
APPLICANT: Bithain, Bernard
APPLICANT: Buthain, Bernard
APPLICANT: Boulett, Aymeric
APPLICANT: Bougoleret, Lydie
APPLICANT: Bougoleret, Lydie
APPLICANT: Bebes-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.022.CIP
CURRENT FILING DATE: 2000-12-28
FRIOR FILING DATE: 2000-06-21
PRIOR PPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR PPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR PPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR PPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
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                               Gaps
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                            Indels
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Best Local Similarity 100.0%; Pred. No. 6.3e-06; Mutches 35; Conservative 0; Mismatches 0;
                                                                                                              8966 GGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 9000
                                                                               77 GGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
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LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
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MAME/KEY: misc.feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                    Sequence 1, Application US/09750580 Patcnt No. 6455280 GENERAL INFORMATION:
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LOCATION: 1239
OTHER INFORMATION: 20-828-311
NAME/KEY: allele
LOCATION: 12347
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NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250
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LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
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LOCATION: 13470..13526 '
OTHER INFORMATION: exon 2
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LOCATION: 12947..12958
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SEQ ID NO 1
LENGTH: 81001
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US-09-750-580-1/c
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APPLICANT:
APPLICANT:
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Conservative
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; LOCATION: (37)...(2442)
US-09-632-098-1
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; ORGANISM: Homo sapiens
US-09-305-384-6
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 34; Conserv
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SEQ ID NO 1
LENGTH: 3431
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LENGTH: 2834
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Patent No. 6242218
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
US-09-798-096-10/C
Sequence 10, Application US/09798096
Fatent No. 6399378
Fatent No. 6399378
FAPLICANT: HOFORMATION:
TILLE OF INVENTION:
FILE REFERENCE: RTS.-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT APPLICATION NUMBER: US/09/798,096
FILE REFERENCE: RTS.-0207
SEQ ID NO 10
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              NAME/KEY: primer_bind
UCCATION: 77039...77057

OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
UCCATION: 77059...77077

OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
UCCATION: 77059...7707

OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
OTHER INFORMATION: 20-823-415.mis complement
NAME/KEY: misc_binding
UCCATION: 1237...1251

OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
UCCATION: 15229...1523

OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
UCCATION: 42206...4230

OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
UCCATION: 45430...45454
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6e-06;
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OTHER INFORMATION: 20-842-115.mis complement
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Matches 35; Conservative
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Matches 35; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09632098
FEREAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Bishop, Paul D.
TILLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REFERENCE: 99-39
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Sequence 3, Application US/09632098
Fatent No. 6420154
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REPERENCE: 99-339
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT APPLICATION NUMBER: US/09/632,098
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Pred. No. 2e-05;
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2.0%; Score 34; DB 4; Le
Eest Local Similarity 100.0%; Pred. No. 2e-05;
Matches 34; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred
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                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
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2e-05;
hes 0; Indels
                                                                           Length 3468;
                                                            DB 4; Lens.
3, 2e-05;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                    3171 GGTGGCTCATGCCTATAATCCCAGCACTTTGGGA 3204
                                                                                                                                                 77 GGTGGCTCATGCCTATAATCCCAGCACTTTGGGA 110
                                                                       Query Match 2.0%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 2e-Matches 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET VUNBER: OKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4773 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             Sequence 9, Application US/08884324 Patent No. 6060283 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahi KURIMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE: ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.0%
Best Local Similarity 100.0
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.4773
IDENTIFICATION METHOD:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
; NAME/KEY: CDS
; LOCATION: (37)...(2472)
US-09-632-098-3
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                                                                                                                                                                                                                                                              US-08-884-324-9
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Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
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                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                               TITLE OF INVENTION: Protein Targeting to Glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: AShbrook, Charles W
REFERENCE/DOCKET NUMBER: 5485-01-CA
TELEPHONE: 313 996-5215
TELEPHONE: 313 996-5215
TELEPEAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Scor.
100.0%; Pred. No. 1.-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,948
FILING DATE: 25-Feb-1999
CLASTEICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,107
                                                                                                                                                                                                                                                  ADDRESSEE: Warner-Lambert Company
STREET: 201 Tabor Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 4238.5176
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                 Printen, John A
Saltiel, Alan R
Warner-Lambert Company,
                 Sequence 3, Application US/09242948
Patent No. 6252057
GENERAL INFORMATION: APPLICANT: Brady, Matthew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 5789 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       CITY: Morris Plains
                                                                                                                                                                                                                                                                                                                                                    ZIP: 07950
COMPUTER READABLE FORM:
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0°
Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
US-09-242-948-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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US-08-884-324-13
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
E: BROWDY AND NEIMARK 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIPLICATION: 435

CLASSIPLICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 185,305/96

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGER L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKURA-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPROSE 202-628-5197

TELEPROSE 202-737-3528

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 11464 base pairs

TYPE: NUCLEIC acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..3

LOCATION: 1..3

LIDENTIFICATION METHOD: E
LOCATION: 4..82

LIDENTIFICATION METHOD: S
LOCATION: 83..1453

LOCATION: 83..1453

LOCATION: 83..1453

LOCATION: 1454..1465

LOCATION: 1454..1465

LOCATION: 1454..1465

LOCATION: 1466..4848

LOCATION: 1466..4848

LOCATION: 1469..486

LOCATION: 1466..4848

LOCATION: 1466..4848

LOCATION: 1466..4848

LOCATION: 1466..4848

LOCATION: 1466..4848

LOCATION: 1466..4848

LOCATION: 4849..4865

LOCATION: 4849..4865

LOCATION: 4866..4983

LOCATION: 4866..4983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE: ORGANISM: human TISSUE TYPE: placenta FEATURE: NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
NAME/KEY: 3'UTR
LOCATION: 11444..11464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat peptide
11225..11443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
NAME/KEY: mat peptide
LOCATION: 6318..6451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6452..11224
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           STREET: 412 CTTY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEAC
STRANDEDNESS:
TOPOLOGY: Line
                                                          STATE: D
COUNTRY:
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RESULT 39
US-09-087-465-3/C

Sequence 3, Application US/09087465A

Batent No. 6160092

GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, Uwe
TITLE OF INVENTION: A GRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
TITLE OF INVENTION: A GRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
CURRENT APPLICATION UNBER: US/09/087,465A

CURRENT FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 37

SOFTWARE PARENT OF THE CORE PORTION OF A STAT AND METHODS OF

SOFTWARE FILING DATE: 1998-05-29
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                                                      Gaps
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Fatent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Masahi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESONDENCE ADDRESS:
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           Length 11464;
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                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8e-05;
hes 0;
      DB 3; L 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 17855 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 17822
                                                                                                             Query Match 2.0%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 34; Conservative 0; Mismatches
                                                                                        78 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILLING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BROWDY AND NEIMARK
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Best Local Similarity 100.0%; P

Matches 34; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 17949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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US-08-884-324-14
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RESULT 43
US-09-345-882-1
US-09-345-882-1
Sequence 1, Application US/09345882
Sequence 1, Application US/09345882
Sequence 1, Application US/09345882
Sequence 1, Application US/09345882
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
CURRENT APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.Pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBENCE: CLOOIL78DIV
CURRENT APPLICATION NUMBER: US/99/978,197
CURRENT FILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                           Query Match 2.0%; Score 34; DB 4; Length 59065; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 34; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 59065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%; Score 34; DB 4; L
100.0%; Pred. No. 1.6e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 DD 13652 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 13685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 13652 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 13685
                                                                                                                                                                                                                                                                                                                                                                    78 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
  CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 59065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 42
US-09-278-197-3
: Sequence 3, Application US/09978197
: Patent No. 6403353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 34; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human US-09-978-197-3
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LENGTH: 162450
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LENGTH: 59065
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US-09-813-817-3

Sequence 3, Application US/09813817

Sequence 3, Application US/09813817

Patent No. 6340583

GENERAL INFORMATION:

APPLICANT: YAN. Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 24033 GIGGCICATGCCTATAATCCCAGCACTTTGGGAG 24066
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                             OKURA-1
                                                                           TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Innear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
REGISTRATION NUMBER: 25,618
REPERENCE/DOCKET NUMBER: OK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: S'UTR
LOCATION: 1..15606
LOCATION HILLS606
LOCATION METHOD: E
NAME/KEY: Leader peptide
LOCATION METHOD: S
NAME/KEY: LIGHTON METHOD: S
NAME/KEY: LINTON
LOCATION METHOD: E
NAME/KEY: LIGHTON
LOCATION METHOD: S
NAME/KEY: LIGHTON
LOCATION: 17057..17068
LOCATION: 17057..17068
LOCATION: 17057..17068
LOCATION: 17057..17068
LOCATION: 17069..20451
LOENTIFICATION METHOD: S
NAME/KEY: LIGHTON
LOCATION: 20452..20468
LOCATION: 20469..20586
LOCATION: 20469..20586
LOCATION: 20469..20586
LOCATION: 20587..21920
LOCATION: 20587..21920
LOCATION: 20587..21920
LOCATION: 20587..21920
LOCATION: 20587..2054
LOCATION: 20587..2064
LOCATION: 20687..2064
LOCATION: 20687..2064
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LOCATION: 20687..2064
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TISSUE TYPE: placenta
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: polymorphic base

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OTHER INFORMATION: 5-143-101
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                           NAME/KET: allele
LOCATION: 150329
OTHER INFORMATION: 5
FEATURE:
NAME/KEY: allele
LOCATION: 160031
                                                                                                                        NAME/KEY: allele
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NAME/KEY: allele
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NAME/KEY: allele
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                                                                                            FION: 90842
R INFORMATION: 99-1437-325
                                                                                                                                                                                         LOCATION: 97122
OTHER INFORMATION: 99-1442-224
                                             LOCATION: 88073
OTHER INFORMATION: 5-127-261
LOCATION: 72794
OTHER INFORMATION: 5-124-273
                                                                                                                                                                                                                                       LOCATION: 97152
OTHER INFORMATION: 5-129-144
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                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 103806
OTHER INFORMATION: 5-131-395
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: 108106
INFORMATION: 5-135-155
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LOCATION: 134134
OTHER INFORMATION: 5-140-120
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NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174
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OTHER INFORMATION: 5-128-60
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LOCATION: 108149
OTHER INFORMATION: 5
FEATURE:
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NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 108308
OTHER INFORMATION:
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INFORMATION:
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OTHER INFORMATION:
                                                                                                                    FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
LOCATION: 146345
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OTHER INFO
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NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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NAME TO SECOND STATES
OTHER INFORMATION: POLYMORPHIC fragment 99-1442-224 SEQ ID71
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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
                                                                                                                                                 LOCATION: 72771...72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
                                                                                                                                                                                                                                    INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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LOCATION: 97130 .97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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LOCATION: 99075..99121
OTHER INFORMATION: Polymorphic fragment 5-130-257 SEQ ID34
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
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OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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    or
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ
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base
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LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144
                                                                                      : polymorphic
polymorphic
                                                                                  5-148-352
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
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n. 0.00016;
0;
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PILLOATION NUMBER: US/09/062,451
PILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                               / Match 1.9%; Score 32; DB 4; L. Local Similarity 100.0%; Pred. No. 0.00016; nes 32; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9%; scc. 100.0%; Pred. No. 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              483 AGCACTTTGGGAGCCTGAGGTGGGTGGATCAC 452
                                                                                                                                                                                                                                                                                                                                                                       99 AGCACTTTGGGAGCCTGAGGTGGGTGGATCAC 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY, FAGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09062451; Patent No. 6344550; GENERAL INFORMATION:
                                                                                                                                LENGTH: 548 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Frudakis, Tony N. APPLICANT: Smith, John M. APPLICANT: Reed, Steven G.
                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 32; Conserva
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                                                                                                                                                                                                                                         US-08-991-789A-15
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US-09-062-451-15
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SPLICANT: Frudakis, Tony N.
Red, Steven G.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 162450;
                                        LOCATION: 103783..103828
OTHER_INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38 FRATURE:
NAME/KEY: allele LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                     FEATURE:
NAME/KEY: allele
COATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ
FEATURE:
                                                                                                                            LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Le
1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 125653 GACGTGGTGGCACACCTGTAATCCCAGCTACT 125686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 GACGTGGTGCACACACCTGTAATCCCAGCTACT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/991,789A
FLING DATE: 11-Dec-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.0%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-991-789A-15/c; Sequence 15, Application US/08991789A; Patent No. 6225054; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 106918..106966
                                                                                                                                                                                                                                                                                                                                                                                         108084..108130
                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: allele
                                                                                                        NAME/KEY: allele
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PC-DOS/MS-DOS
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US-09-851-896-3/c
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US-09-128-155-17
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US-09-851-896-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                        ADDRESSEE: Seed Intellectual Property Law Group PLLC STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 548;
                                                                                                                                                                                                                                                                                                                                     COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,326
FILING DATE: 20-Jun-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: POÈLEE., Jane Er.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 AGCACTTTGGGAGCCTGAGGTGGGTGGATCAC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 AGCACTTTGGGAGCCTGAGGTGGGTGGATCAC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
APPLICANT: Sadlacek, Hans-Harald
TITLE OF INVENTION: PREMATION OF TITLE OF INVENTION: PREPARATION AND USINGHESPONDENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                         Sequence 15, Application US/09598326
Patent No. 6423496
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09039555B Patent No. 6033856
                                                                             APPLICANT: Frudakis, Tony N. Smith, John M. Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15
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                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                     STATE: Washington
                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
                                                                                                                                                                                                                                                                    CITY: Seattle
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3000 K S. CITY: Washington STATE: D.C.
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US-09-039-555B-19/C
    US-09-598-326-15/c
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APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTIESSENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEP
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,555B
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9%; Score 32; DB 4; L. 100.0%; Pred. No. 0.00011; iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913 GTGGTGCACACCTGTAATCCCAGCTACTT 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
                                                                                CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19710643.9
FILING DATE: 14-WAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016779/0131
TELECHONE: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGHH: 2000 base pairs
TYPE: nucleic acid
STRANDENESS: 51ngle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9%; Score 32;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                          016779/0131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09851896; Fatent No. 6410325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.9
Best Local Similarity 100.
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 32; Conservative
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RESULT 50
US-09-183-266A-12/C
Sequence 12, Application US/09183266A
Patent No. 6361954
GENERAL INFORMATION:
APPLICANT: Stillman, Bruce
APPLICANT: Williams, R. Sanders
TITLE OF INVENTION: DAN REPLICATION TO AN ANTIBODIES THERETO AND DIAGNOSTIC APPLICATIONS THEREOF
FILE REFERENCE: CSLL98-10-30
CURRENT FILING DATE: 1998-10-30
PRIOR FILING DATE: 1997-05-12
PRIOR APPLICATION NUMBER: 08/648,650
PRIOR APPLICATION NUMBER: 08/648,650
PRIOR PLICATION NUMBER: 08/643,034
PRIOR FILING DATE: 1996-05-15
PRIOR FILING DATE: 1996-05-05-15
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
TAYPE: DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 127041 GGCTCATGCCTATAATCCCAGCACTTTGGGAG 127072
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
FEARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
SARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PSALSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 GGCTCATGCCTATAATCCCAGCACTTTGGGAG 111
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NAME/KEY: misc_feature

LOCATION: (1)...(176373)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: H. sapiens
US-09-183-266A-12
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Search completed: February 12, 2003, 16:27:34 Job time: 2065 secs

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		~	Sequence 2718, Ap Sequence 1471, Ap Sequence 1850, Ap Sequence 18, Appl										Sequence 3, Appli Sequence 314, App Sequence 9244, Ap Sequence 7719, Ap											Sequence 2956, Ap Sequence 774, App Sequence 773, App		Sequence 5, Appli Sequence 292, App
													US-09-810-6/3A-3 US-09-967-768A-314 US-09-867-701-9244 US-09-867-701-719					US-09-734-674-3 US-09-867-701-9236			US-09-969-347-293 US-09-867-701-8177	US-10-920-300A-1579 US-10-033-528-1579				
65464 9 76798 1 111282 1	145831 1	2791 5815 7373	9968 1 10322 9 13069 1 27377 1	28770 1 32203 1 51719 1	84539 1 92139 1	110096 1 349 1 425 1	1788 1 8082 1	32190 1 26048 1	143068 1 167343 1	293 1 438 1	643 1 1174 1 8220 1	11469 1 22484 1 22484 1 26657 1	-	1282 1 4457 1	20522 1 20522 1 23071 1 28818 1	30013 1 49744 1 52354 1	99014 1 106323 1 15233 9	202001 1 309 1	321 1	378 1	388 1	397 1	451 1	903 1779 1780	1988 1 6040 1	6235 6427
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		<b>₩</b> ← ←	tc				22880			COMB.seq:*	PUB.seq:* _PUB.seq:* COMB.seq:*	FVB.seq:* BCOMB.seq:* PVB.seq:*	COMB. Seq: * PUB. Seq: * BCOMB. Seq: * W_PUB. Seq: *	W_PUB.seq:* BCOMB.seq:*	chance to have result being pristribution.		Descripti	S					Sequence			S
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10 US-09-867-701-8012 Sequence 10 US-09-880-107-1880 Sequence 10 US-09-969-347-113 Sequence	10 US-09-880-107-1402 Sequence	9 US-09-954-531-1316 Sequence	10 US-09-960-352-7819 Sequence	10 US-09-867-701-7901 Sequence	10 US-08-80/-/01-9089 Seduence	10 03 03 00/ /01 / 323 Sequence	10 CO	10 03-00-00-101-3003	10 US-US-880-10/-2480 Sequence	9 US-09-946-807-324 Sequence	9 US-09-946-807-832 Sequence	9 US-09-946-807-937	9 11S-04-946-807-1087		10 US-09-793-000-324 Sequence	TO 05-09-795-668-832 Sednence	10 US-09-795-668-937 Sequence	10 US-09-795-668-1087 Seguence	10 115-00-705-696-374	10 03-03-131-000-324 Seduence	10 US-09-795-686-832 Sequence	10 US-09-795-686-937 Sequence	10 rrs-09-795-686-1087 Sections	00 00 00 00 00 00 00 00 00 00 00 00 00	TO 02-03-20/-/OT-/202 Sedneuce	10 US-09-815-343-441 Sequence	10 IIS-09-867-701-8568	מפיל שנו איז מים איז מים	9 US-U9-346-8U/-14U3 Sequence	10 US-09-795-668-1403 Sequence	10 rrs-00-795-686-1403	10 03 03 133 060 T403 Seduence	10 US-09-783-590-11905 Sequence	10 US-09-867-701-10648 Segmence		10 US-09-86/-/01-5629 Sequence	9 US-10-040-739-1025 Sequence	9 US-09-764-868-1302 Seguence	1010 TO 1010 T	9 US-U9-/04-808-1303 Sednence	10 US-09-867-701-10152 Sequence	10 10 10 10 10 10 10 10 10 10 10 10 10 1	TO OS-08-80/-/OI-8850 OT	10 US-09-867-701-4136 Segmence	10 115-00-867-701-8582		TO 02-03-80'-/01-//90 Sedneuce	9 US-09-796-692-7801 Seguence	10 119-09-867-701-277		acinemica one not to the seducine	10 US-09-867-701-2993 Sequence	10 US-09-867-701-10007 Sequence	10 118-09-764-878-402		TO 02-03-00/-/0T-3300 pedmence	10 US-09-880-107-454 Sequence	10 US-09-867-701-3633 Seguence	10 march 01	2011-101-101 Seducince	10 US-09-867-701-6777 Sequence	9 119-09-854-133-109		TO D2-03-138-109 Sedneuce	10 US-09-867-701-6700 Sequence	0 115-00-706-602-3670		In US-US-920-300A-148/ Sequence	12 US-10-033-528-1487 Sequence	10 US-09-827-998-59	10 115-00-867-701-1208	10 00 01 101 1230 Sequence	TO US-US-BI/-ISBA-I4 Seduence	10 US-09-783-590-5651 Sequence	10 US-09-867-701-876 Seguence	9 115-10-046-935-1395		9 US-U9-8/8-I/8-I395 Sequence	9 US-09-796-692-7184 Sequence	10 HS-09-764-847-1069	מפלות מולי לפל לפל לפל לפל לפל לפל לפל לפל לפל ל	8 0S-09-796-692-8715 Sednence	10 US-09-764-847-1841 Sequence	10 115-09-754-847-1071 Coduence	10 US-09-764-847-10/1 Sequence	10 US-09-764-847-1072 Sequence	
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APPLICANT: GOOGLICH, KYLE
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Dang, Jian-Rui
APPLICANT: Dang, Jian-Rui
APPLICANT: Dang, Jian-Rui
APPLICANT: Dang, Jian-Rui
APPLICANT: Demanac, Radoje T.
TITLE OF INVENTION: No. US20020061567Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2C
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PRING DATE: 2000-08-23
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                       Length 65464;
                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 47; DB 10; Length 776; 100.0%; Pred. No. 1.7e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             220 CCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
                                                                                                                                                                                                                                                                                                     2.9%; Score 48; DB 9; Length 654
100.0%; Pred. No. 3e-08;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001239
CURRENT APPLICATION NUMBER: US/09/859,888
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                   ; LUCATION: (1)...(65464); OTHER INFORMATION: n = A,T,C or GUS-09-859-888-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-728-711-7; Sequence 7, Application US/09728711; Fatent No. US20020061567A1
; ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/10161510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 48; Conservative
                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (147)...(446) US-09-728-711-7
                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                  SEQ ID NO 3
LENGTH: 65464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-161-510-1/c
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Patent No. US20020173459A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YAN, Chunhus et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBENC: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3251
LENGTH: 32177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 32177;
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US-10-175-737-11
US-09-993-667-27
US-10-175-738-12
US-10-175-738-11
US-10-175-738-11
US-10-176-752-11
US-10-176-757-11
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US-10-180-557-11
US-10-180-557-11
US-09-997-428-27
US-09-997-428-27
US-09-997-428-27
US-09-997-458-21
US-10-174-572-11
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US-10-175-743-11
US-10-175-743-11
US-10-175-743-11
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US-10-176-488-11
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US-10-176-78-11
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US-10-176-992-11
US-10-176-993-11
US-10-184-658-11
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US-10-176-987-11
US-10-176-991-11
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                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3251
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Best Local Similarity
'-hac 49; Conserva
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ORGANISM: Homo sapien
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US-09-962-832-154/c
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US-09-867-701-7324
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                                                                      SEQ ID NO 8121
LENGTH: 397
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                                                                                                                      TYPE: DNA
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                                      APPLICANT: EXELIXES, INC.
TITLE OF INVENTION: PIBS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REPRENCE: EXO2-074C
CURRENT APPLICATION WHBER: US/10/161,510
CURRENT PILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-15
NUMBER OF SEQ ID NOS: 14
SUPPLY FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 14
SUPPLY FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 14
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APPLICANT: KUMAGAI, Akiko
APPLICANT: KUMAGAI, Akiko
TITLEOMY: UNDMPHY, WIlliam
TITLEOF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
FILE REFERENCE: CIT1320-1
CURRENT APPLICATION NUMBER: US/09/982,091A
CURRENT FILING DATE: 2002-10-17
PRIOR FILING DATE: 2000-10-17
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Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
ITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
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CURRENT APPLICATION NUMBER: US/09/867,701
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Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 43; Conservative 0; Mismatches 0;
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Publication No. US20020192695A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo sapiens
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US-09-867-701-8121/C
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LENGTH: 133893
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US-09-982-091A-5/C
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LENGTH: 58837
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Sequence 154, Application US/09962832

Fatent No. US20020110821A1

Fatent No. US20020110821A1

Fatent No. US20020110821A1

Fatent No. US20020110821A1

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign

TITLE OF INVENTION: US/09/962,832

FILE REFERENCE: 689290-74

CURRENT PILING DATE: 2001-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

NUMBER OF SEQ ID NOS: 259

SOFTWARE: Patentin version 3.0

SEQ ID NO 154

LENGTH: 302250
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APPLICANT: Harlocker, Susan L,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/667,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7324
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2.3e-06;
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Pred. No. 9.3e-06;
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100.0%; Pred. No. ...
... 0; Mismatches
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CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US/002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
                                                                                                                                                                                    NAME/KEY: misc_feature
COATION: (1)...(397)
COTHER INFORMATION: n - A,T,C or
US-09-867-701-8121
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C TITLE OF INVENTION: Sets
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FILE REFERENCE: 689209-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PRIOR DATE: 2000-09-26
PRIOR PRIOR DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
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Pred. No.
  PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
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; Patent No. US20020115057A1
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100.0%; Pre
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                                                                                                            NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-45
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APPLICANT: Young, Paul
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Best Local Similarity
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US-09-969-347-234
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                                                                                                                                                         SEQ ID NO 45
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Fatent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-01-02
SOFTWARE: PATENTIN NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z28339
US-09-880-107-3872
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                                             Length 400;
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1.4e-05;
                                          DB 10;
. 2e-05;
                                        Score 41; DB 1; Pred. No. 2e-(0; Mismatches
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100.0%; Pred. No. 1.4
rative 0; Mismatches
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PRIOR FILING DATE: 2000-09-27
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                        2.4%; Sco.
100.0%; Pre
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Best Local Similarity 100.0
Matches 41; Conservative
                                                                                     Conservative
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                    Query Match
Best Local Similarity
US-09-867-701-7324
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LENGTH: 2694
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US-09-954-456-45
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US20020115085A1

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                                                                                                                                                                                                                                                                                        Sequence 322, Application US/09764855
Patent No. US20020119919A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA110
CURRENT APPLICATION NUMBER: US/09/764,855
CURRENT APLICATION NUMBER: US/09/764,855
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 334
SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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                                                             Query Match
2.4%; Score 41; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 41; Conservative 0; Mismatches 0;
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Pred. No. 9.3e-06;
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100.0%; Pred. No. 9.3e-
-+ive 0; Mismatches
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100.0%; Pred. No. oc...
... 0; Mismatches
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Best Local Similarity 100.0
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; ORGANISM: Homo sapiens
US-09-764-877-3806
; ORGANISM: Homo sapiens US-09-764-855-321
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ORGANISM: Homo sapiens
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US-09-764-855-322/c
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LENGTH: 16552
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LENGTH: 18878
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US-09-835-081-3
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           GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-69
CURRENT APPLICATION NUMBER: US/09/969,347
CURRENT FILING DATE: 2001-10-02
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SEQ ID NOS: 318
SEQ ID NO 234
LENGTH: 3088
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Patent No. US20020094953A1

GENERAL INFORMATION:

APPLICATTON:

TITLE OF INVENTION: NUMBER:

FILE REFERENCE: PC008

CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1198

SOFTHARE: PatentIn Ver. 2.0

SEQ ID NO 1091

LENGTH: 15500
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Patent No. US20020119919A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAll0
CURRENT APPLICATION NUBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
FILD APPLICATION NUBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
FILD APPLICATION NUBER: US/09/764,855
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: DAA
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100.0%; Pred. No. 9.4e-06;
Live 0; Mismatches 0;
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Best Local Similarity 100.0
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; ORGANISM: Homo sapiens
US-09-969-347-234
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US-09-764-860-1091
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US-09-764-860-1091/c
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GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-W0.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
NUMBER OF SEQ ID NOS: 3950
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; Patent No. US20020142981A1
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; OTHER INFORMATION: n = A,T,C or G
US-09-859-888-3
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Best Local Similarity 100.0%; P:
Matches 41; Conservative 0;
                                                      ; LOCATION: (1)...(58985)
; OTHER INFORMATION: n = A,T,C or
US-09-901-152-3
                                                                                                                                                                                             41; Conservative
                                 NAME/KEY: misc_feature
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Best Local Similarity
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US-09-880-107-3949/c
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US-09-859-888-3
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PUblication No. US20030022824A1
GENERAL INFORMATION.
GENERAL INFORMATION.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001248
CURRENT FILING NAMBER: US/09/901,152
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 5
SSCTUARE FASTSEQ for Windows Version 4.0
LENGTH: 58985
                  TITLE OF INVENTION: ISOLATED HOMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILLE REFERENCE: CLO01224
CURRENT APPLICATION NUMBER: US/09/835,081
CURRENT FILLIG DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWAKE: FASTSEQ for Windows Version 4.0
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Patent No. US20020151030A1
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: DUNBHY, WILLiam
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
FILE REPERENCE: CIT1320-1
CURRENT APPLICATION NUMBER: US/09/982,091A
CURRENT APPLICATION NUMBER: US 60/241,246
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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100.0%; Pred. No. 7.1e-06;
tive 0; Mismatches 0;
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2.4%; Score 41; DB 10; I
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 41; Conservative 0; Mismatches 0;
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APPLICANT: YAN, Xianghe et al
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Best Local Similarity 100.0
Matches 41; Conservative
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SOFTWARE: PatentIn version
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; ORGANISM: Human
US-09-835-081-3
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ORGANISM: Human
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LENGTH: 58837
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                                                                                                                                                                                                         SEQ ID NO 3
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Sequence 3, Application US/09859888
Fateri No. US20020173459A1
FATERI NFORMATION:
TITLE OF INVENTION: ISOLAFED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILLE REFRENCE: CLOO0129
CURRENT APPLICATION NUMBER: US/09/859,888
CURRENT FILING DATE: 2001-05-18
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   Length 58985;
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                                                                                       Db 15004 GGGTGCGGTGCCTCATGCCTATAATCCCAGCACTTTGGGAG 14964
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 DB 9; Le
. 7.1e-06;
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Pred. No. 6.9e-06;
0; Mismatches 0;
2.4%; Score 41; DB 100.0%; Pred. No. 7.1 tive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 65464
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FARENT NO. US.OUZ.LISOS.ALI
FARENT NO. US.OUZ.LISOS.ALI
FARENT NO. US.OUZ.LISOS.ALI
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
ITILE OF INVENTION: Sets
FILE REFERENCE: 689290.76
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
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                                                                              Db 10106 TCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 10066
                                          227 TCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAA 267
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5.9e-06;
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FILING DATE: 2000-09-27
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; Patent No. US20020115057A1
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SOFTWARE: PatentIn version 3.0
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US-09-969-708-79
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US-09-954-456-2116/c
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US-09-969-708-79/c
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US-09-804-474A-3/C
US-09-804-474A-3/C
Sequence 3, Application US/09804474A
Patent No. US20020119518A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/09/804,474A
CURRENT APPLICATION UNMBER: US/09/804,474A
SOUTHEND SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3

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APPLICANT: WEI, MING-HUI et al
APPLICANT: WEI, MING-HUI et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PROSPHODIESTERASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOOJOG3DIV
CURRENT APPLICATION NUMBER: US/10/094,989
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/754,250
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                                                                   Length 76798;
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                                                                                                                                                                                                                                          Db 28999 GGGTGGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAG 28959
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Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 41; Conservative 0; Mismatches 0;
                                                                   Query Match 2.4%; Score 41; DB 10; I Best Local Similarity 100.0%; Pred. No. 6.7e-06; Matches 41; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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: LCCATION: (1)...(111282)

: OTHER INFORMATION: n ~ A,T,C or G

US-10-094-989-3
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OTHER INFORMATION: n = A,T,C or G
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Patent No. US20020115179A1
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Matches 41; Conservative
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US-09-880-107-3949
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Length 2791;

2.9e-05;

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220 CCTGTAATCCCAGCTACTTAGGAGGCTGAGGCAGGAGAAT 259
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100.0%; Pri
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Best Local Similarity 100.0%; P
Matches 40; Conservative 0;
                  2000-12-04
                                                                                                NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 2791
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Matches 40; Conservative
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US-09-764-847-1487
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               CURRENT FILING DATE:
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US-09-764-853-896/C
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US-09-729-674-51
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LENGTH: 5815
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Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: HORNE, Darci T.

APPLICANT: Gene Logic, Inc.

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

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                                                                                                                                                                                 Score 41; DB 10;
Pred. No. 5.9e-06;
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Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 40; Conservative 0; Mismatches 0;
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100.0%; Pred. No. ...
... 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/729,674
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Steininger II, Robert J.
Spaulding, Vikki
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LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                          Query Match 2.4%
Best Local Similarity 100.(
Matches 41; Conservative
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Merberg, David
Treacy, Maurice
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Clark, Hilary
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                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2116
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ORGANISM: Homo sapiens
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US-09-880-107-832/c
SEQ ID NO 2116
LENGTH: 145831
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APPLICANT:
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APPLICANT:
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                                                                                                                            FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: D206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 896
US-09-764-847-1487/c
Sequence 1487, Application US/09764847
Fatent No. US20020132767A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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100.0%; Pred. No. 2.4e-05.
ve 0; Mismatches 0
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Pred. No.
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Sequence 18, Application US/09816248
Patent No. US20020137703A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAUMANN. BETER
APPLICANT: CECH, THOMAS R.
TITLE OF INVENTION: POLYNUCLEOTIDES
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: 08491/0201
CURRENT APPLICATION NUMBER: US/09/816,248
CURRENT APPLICATION NUMBER: US/09/816,248
SOFTWARE: PATENTIN VAI: 2.1
SEQ ID NO 18
LEGGTH: 27377
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Patent No. US20020146758A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO0118
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT PILLING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                Length 13069;
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100.0%; Pred. No. 1.8e-05;
Live 0; Mismatches 0;
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Best Local Similarity 100.(
Matches 40; Conservative
                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1850
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; ORGANISM: Homo sapiens
US-09-816-248-18
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Best Local Similarity
Matches 40; Conserva
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; ORGANISM: Human
US-09-817-198A-3
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       LENGTH: 13069
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                                                              RESULT 30
US-00-764-877-2718
Sequence 2718, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT FPLLION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2718
LENGTH: 9968
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Sequence 1471, Application US/09764868

Patent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies

TITLE OF INVENTION: NUMBER: US/09/764,868

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT FILING DATE: 2001-01-17

FILOR application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 1510

SEQ ID NO 1471

LENGTH: 10322
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Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9968;
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2.2e-05;
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2.2e-05;
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100.0%; Pred. No. 2.
... 0; Mismatches
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Best Local Similarity 100.
Matches 40; Conservative
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US-09-764-868-1471
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APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer; FILE REFERENCE: 44921-5028-W0.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                       Length 84539;
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Pred. No. 1.4e-05;
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100.0%; Pred. No. ...
0; Mismatches
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APPLICANT: Proll, Sean
APPLICANT: Proll, Sean
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
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100.0%; Pred. No. 1.
... 0; Mismatches
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NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
    PRIOR APPLICATION NUMBER: US/60/235,082 PRIOR FLILNG DATE: 2000-09-25 PRIOR APPLICATION NUMBER: US/60/234,924 PRIOR FILING DATE: 2000-09-25 NUMBER OF SEQ ID NOS: 568 SOFTWARE: Patentin version 3.0 SEQ ID NO 36
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; Patent No. US20020076720A1
; GENERAL INFORMATION:
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LOCATION: 7043, 8369, 8401
OTHER INFORMATION: n = A,T,C or G
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Matches 40; Conservative
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                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                              LENGTH: 84539
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US-09-918-686-1/c
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
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                                                           GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                       Length 32203;
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1.6e-05;
thes 0;
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APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Paeper, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001.07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
                      Sequence 1849, Application US/09764869 Patent No. US20020061521A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/09962436 Patent No. US20020081301A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LCCATION: 1246, 2572, 2604
CTHER INFORMATION: n = A,T,C or G
US-09-918-686-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09918686 Patent No. US20020076720A1
                                                                                                                                                                                                                                                                                                         TYPE: DNA; ORGANISM: HOMO SapienS
US-09-764-869-1849
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US-09-764-869-1849/c
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LENGTH: 32203
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US-09-918-686-2/C
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Conservative
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US-09-822-830A-569
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Matches 39; Conserv
                                     RESULT 42
US-09-822-830A-569/c
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US-09-764-860-1106
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                                                                                                                       ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AD000092
US-09-880-107-1542
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2735, Application US/09764877

Patent No. US20020147140a1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2735

LENGTH: 349
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Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2736

LENGTH: 425
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1.4e-05;
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. 9.9e-05;
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9.5e-05;
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Best Local Similarity 100.(
Matches 39; Conservative
                    PatentIn Ver. 2.1
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NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2..
SEQ ID NO 1542
LENGTH: 110096
                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2735
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; ORGANISM: Homo sapiens
US-09-764-877-2736
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Best Local Similarity
Matches 39; Conserv
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US-09-764-877-2736
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                                                                                           APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Techtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Stewen H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Ramblakar
APPLICANT: Gulukota, Kamblakar
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT APPLICATION NUMBER: US/09/822,830A
PRIOR REPLING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-06
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Fatent No. US20020094953A1

GENERAL INFORMATION:
FAPLICANT: ROSEN et al.
TITLE OF INVENTION:
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1198

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 1106

LENGTH: 8082
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100.0%; Pred. No. 5.1e-05;
tive 0; Mismatches 0;
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Pred. No. 7e-05;
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; Sequence 569, Application US/09822830A
patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
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; Patent No. US20020061521A1
; GRNERAL INFORMATION:
; APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 631
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 569
LENGTH: 1788
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; Sequence 281, Application US/09962436

; Patent No. US20020081301A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign

; TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Sets
FILLE REFERENCE: 689290-73
CURRENT PAPLICATION NUMBER: US/09/964,824A
CURRENT PAPLICATION NUMBER: US/09/964,824A
CURRENT PAPLICATION NUMBER: US/06/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: PAPLICATION NUMBER: US/60/236,028
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hes 0;
                                                                           2.3%; Score 38; DB 10;
100.0%; Pred. No. 6.1e-05;
tive 0; Mismatches 0;
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Pred. No. 5.9e-05;
); Mismatches 0;
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Hismatches
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CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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; Patent No. US20020102531A1
; GENERAL INFORMATION:
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100.0%; Pre
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Best Local Similarity 100.0%; P
Matches 38; Conservative 0;
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SOFTWARE: PatentIn version 3.0
                                                                                                   Best Local Similarity 100.
Matches 38; Conservative
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Best Local Similarity
Matches 38; Conserv
                  US-09-967-768A-316
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LENGTH: 167343
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US-09-964-824A-273
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                                                                              Query Match
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Patent No. US20020150877A1

GENERAL INFORMATION:

APPLICANT: Augustus,

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE SEFERENCE: 689290-72

CURRENT FILING DATE: 2001-09-28

PRIOR PILING DATE: 2000-09-28

PRIOR PILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

SOFTWARE: PAPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

SOFTWARE: PATENTH VERSION 3.0

SEQ ID NO 316
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1556, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                 2.3%; Score 39; DB 10; I
100.0%; Pred. No. 3.8e-05;
Live 0; Mismatches 0;
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llarity 100.0%; Pred. No. 8.7e-05;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2209
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US-09-764-869-1556
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Best Local Similarity
Matches 38; Conserv
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; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2.001-01-17
; Prior application data removed - refer to PALM or file wrapper; NUMBER OF SED ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SED ID NO 376
; LENGTH: 293
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Fatent No. US20020132237A1
GENERAL INFORMATION
APPLICANT: AJalate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
ATILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT FILING DATE: 2001.05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5962
LENGTH: 438
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Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 37; Conservative 0; Mismatches 0;
2.2%; Score 37; DB 10; 100.0%; Pred. No. 0.00049; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 GTCAGGAGTTCAAGACTAGCCTGGCCAACATGGTGAA 235
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Job time : 1926 secs
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COCATION: (287)
COTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-376
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Matches 37; Conservative
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ORGANISM: Homo sapiens
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US-09-867-701-5962
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US-09-867-701-5962
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US-09-764-877-376
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 364)

S Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

L Onpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                      BG434724 602507926
AQ752230 HS_5572_B
BF794559 602256853
BM79755 AGENCOURT
BM548499 AGENCOURT
AQ756322 HS_5201_B
AQ433028 HS_5148_B
B1491471 df10a02.w
AW020452 df10a02.w
AW020452 AF10805
AV718985 AV718985
AV718985 AV718985
                                    AA595144 n184a11.s
BF819673 MR1-RT002
A1970561 wr12409.x
B6990678 RC4-HT109
AW103010 xd41h11.x
                                                                                                                                                                A2518820 RPCI-11-3
A0897411 HS_3153_A
AA131088 Z501604.s
AQ581201 RPCI-11-4
A1561147 tq37405.x
A1065029 HA0859 Hu
AG035121 PRDI Lrog1
AQ415537 RPCI-11-1
AL700218 DKFZp686N
 AG123613 Pan trog1
AQ394280 CITBI-E1-
AW880489 QVO-OTO03
AW846743 QV3-CT019
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CITBL-E1-2576K5.TF CITBI-E1 Homo sapiens genomic clone 2576K5, DNA
                                                                                     AA326336 EST29495
AA484273 ne88908.s
AA041276 zf08b03.s
AA484304 ne89h08.s
BH610078 HIV20A05
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Clones are available from Research Genetics (info@resgen.com). BAC
and search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3-21
                                                                                                                                              AI811345 tw38f06.x
AL699717 DKFZp686C
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                                               BF819673
AI970561
BG990678
AW103010
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AG035121
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AQ428360
AQ428360.1 GI:4496126
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KEYWORDS
SOURCE
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BF95584 CM0-NN024
N74947 za45905.s1
AQ006763 CIT-HSP-2
B76188 RPCIII-1301
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                                                                February 10, 2003, 20:51:09; Search time 147.133 Seconds (without alignments) 5613.764 Million cell updates/sec
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Maximum Match 100%
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                                               nucleic search, using sw model
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Minimum | Maximum |

Database

Result No.

Searched:

source

FEATURES

Query Match Best Local (

Matches

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BASE COUNT ORIGIN

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location, 1.194
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0249"
/dv.stage="Adult"
/note="Organ: nervous_normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwing Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

48 c 50 g 35 t
                                                                                                                                                                                                                                                                                       Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N74947 227 bp mRNA linear EST 29-MAR-1996 za45g05.sl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:295544 3' similar to contains Alu repetitive element; contains element PTR7 repetitive element; mRNA sequence.
                                                                                                                               EST 22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpsonelludwig.org.br
This sagence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=CMO&t2=CMO-NNO249-181100-710-e09&t13=2000-11-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 194.
                                                                                                                          BF955584 181100-710-e09 NN0249 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 0.00028;
1; Mismatches 4; Indels 0;
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20202663
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            52
    2 TCAAGACCAGCCTGTACAACTTGGAAGAACCCGGTCTCTACAAAAATACA
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                                                                                                                                                                                                BF955584.1 GI:12372859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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SOURCE
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                                                                          RESULT 3
BF955584
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N74947/c
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CITBI-E1-2576P11.TF CITBI-E1 Homo sapiens genomic clone 2576P11,
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                            /cell_type="sperm"
/cell_type="sperm"
/note="Vector: pBeloBACl1; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
on 98 q 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1; CalTech Human BAC Library D" 98 c 123 g 94 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAATACA 51
                                                                                                                                                                                                                                                                                                                                         Length 364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_GSSS: CITEL.1-2576Pll.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2576K5"
/clone_lib="CITBI-E1"
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/sex="male"
                      Location/Qualifiers
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AQ424894.1 GI:4498160
                                                                                                                                                               /sex="male"
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Class: BAC ends.
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Best Local Similarity
Matches 49; Conserv
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SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

DEFINITION

RESULT 2 AQ424894 ACCESSION VERSION KEYWORDS ó;

Gaps

source

FEATURES

BASE COUNT

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USA

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422 bp DNA linear GSS 08-APR-1999
RPCIII-13016.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13016,
DNA sequence.
                                                                                                                                                         Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Ml3 Reverse
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linhcr, K., Golden, J.C. Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter Use of BAC End Sequences for Sequence-Ready Map Bullding
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu/Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
Class: BAC ends.
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/note:"Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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        The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, 1819 1301 838 0200 Fax: 301 838 0208
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Fax: 301 838 0208
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Pred. No. 0.00029;
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Other GSSs: RPCI11-13016.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .465
/organisma"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone."2291F2"
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/sex:"Male"
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/db_xref="taxon:9606"
/clone="libe"Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/dev_stage="20 week-post conception"
/de
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 227)

4 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.,

The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washigton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 465). (bases 1 to 465). (consistent of the consistent of the consistent
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CIT-HSP-2291F2.TR CIT-HSP Homo sapiens genomic clone 2291F2, DNA
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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: ml3 -40 forward
High quality sequence stop: 205.
Location/Qualiflers
1. .25
/organism."Homo sapiens"
/db_xref."GDB:1240465"
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Pred. No. 0.00028;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-133F03.F.
Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-2 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                      GSS 04-NOV-2001
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Pan troglodytes DNA, clone: PTB-133F03.F, genomic survey sequence.
AG123613
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Yector: pBAc63.6; Site_l: EcoR1; Site_2: EcoR1;
RPCIII_Human Male BAC Library"
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 646)
Fullyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                              /sol_type"lymphoblast"
/coll_type"lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
139 c 138 g 167 t 2 others
                                                                                                                                       Length 422;
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Pred. No. 0.00069;
0; Mismatches 5;
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90.2%; Pred. No. 0.0007;
iive 0; Mismatches 5
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-133F03.F"
                                                                                    104 g
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                    84.3%;
90.2%;
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                                                                                                                                                                    Conservative
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AQ394280 147 bp DNA linear GSS 06-MAR-1999 CITBI-E1-2546J24.TR CITBI-E1 Homo sapiens genomic clone 2546J24,
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Venter, J.C.
Venter, J.C.
Ves of BaAC End Sequences from CalTech Libraries for Sequence-Ready Unpublished (1997)
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QVO-COT0030-120500-219-g11 OT0030 Homo sapiens CDNA, mRNA sequence.
AW880489.1 GI:8042499
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1 (bases I to 149)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BACend search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147)
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
1 41 c 33 g 28 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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                                                                                                                                                                                                          AQ394280.1 GI:4365303
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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Conter Clone distribution: NCI-GGAP clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
Insert Length: L155 Std Brror: 0.00
Seq primer: -40ml3 fwd.ET from Amersham
High quality sequence stop: 219.
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl~&t2 QV3-CT0194-051
099-003-c12&t3~1999-10-05&t4~1)
Seg primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 227)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA595144 12. CGAP_Br2 bp mRNA linear EST 25-SEP-15 nl84all.sl NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1057340 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; ', mRNA sequence.
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88.2%; Pred. No. 0.0009;
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/clone_lib."NCI_CGAP_Br2"
/scx."female, proled"
/tissue_typer."brast"
/lab_hoste."DH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                            /organism¬"Homo sapiens"
                                                                                                         High quality sequence stop: 159
                                                                                                                                         Location/Qualifiers
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AA595144/C
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KEYWORDS
SOURCE
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                                                                                                                                         FEATURES
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                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPDSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-OT0030-120 500-219-gll&t3~2000-05-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 149.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 .716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW846743 110-MAY-2000 OV3-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-051099-003-CI0194-05109-003-CI0194-05109-003-CI0194-05109-003-CI0194-05109-003-CI0194-05109-003-CI0194-05109-05109-003-CI0194-05109-003-CI0194-05109-003-CI0194-05109-003-CI0194-05109-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-05-CI0194-
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1 (bases I to 159)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 0.0009;
1; Mismatches 5;
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/db_xref="taxon:9606"
/clone_lib="070030"
/dev_stage="Adult"
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Fax: +55-11-2707001
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//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: kidney_tumor; Vector: pucl8; Site_1: SmaI;
//site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                    ыкв196/3
MR1-RT0028-101100-002-e10 RT0028 Homo sapiens CDNA, mRNA sequence.
BF819673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MRI&t2=MRI-RT0028-101100-002-e10&t3=2000-11-10&t4=1)

Seq primer: puc 18 forward
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 246)
RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI_CGAP_BRI1.1 Library was constructed by Bento Soares and W Estima Ronald. "
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                     Length 227;
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                                                                                                                                                                       Score 42.6; DB 9;
Pred. No. 0.00091;
1; Mismatches 5;
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/db_xref="taxon:9606"
/clone_lib="RT0028"
                                                                                       Fatima Bonaldo.
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High quality sequence stop: 246.
Location/Qualifiers
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88.2%;
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Best Local Similarity 88.2
Matches 45; Conservative
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Score 42.6; DB 12; Length 246; Pred. No. 0.00091; L: Mismatches 5; Indels 0;

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83.5%;

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Ilssue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 346 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 267.
                                                                                                                                                                                                                                                                                                                                                       A1970561 268 bp mRNA linear EST 08-MAR-2000 wrl2a09.xl NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2481304 3' similar to contains Alu repetitive element;contains LTR5 repetitive
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//lab_host="DH10B (phage-resistant)"
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1 (Dases 1 to 268)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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88.2%; Pred. No. 0.00092;
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/clone_lib="NCI_CGAP_Lu19"
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/organism="Homo sapiens"
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Search completed: February 11, 2003, 03:31:06 Job time : 151.133 secs
          Tumor Gene Index
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Best Local Similarity
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/db_xrefo"taxon:9606"
/db_xrefo"taxon:9606"
/done_libo"HT1092"
/dev_stage="Adult"
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_1: Smal; A mini-library was made by cloning products
Site_2: Loudwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                         Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC4&t2=RC4-HT1092-250101-022-b05&t3-2001-01-25&t4-1)

Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence start: 15
High quality sequence store: 196.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 274)
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AWI03010
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NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Llarity 88.2%; Pred. No. 0.00092;
Conservative 1; Mismatches 5; Indels 0;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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75 c 81 g 48
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Laboratory of Cancer Genetics
BG990678
BG990678.1 GI:14394748
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Lumbolished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Not.CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 297.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note:"Organ: ovary; Vector: pCMV-SPORT6; Site_1: Salf; Site_2: Not1; Cloned uniddrectionally. Primer: Oligo dr. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
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/clone_lib="NCI_CGAP_ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
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Pred. No. 0.00092;
1; Mismatches 5;
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/organism~"Homo sapiens"
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Sequence Sequence Sequence

Sequence 79, Sequence 3, A Sequence 10, Sequence 10,

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Sequence 7, A Sequence 7, A Sequence 18, A Sequence 3, A Sequence 3, A Sequence 3, A

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Sequence 35, Sequence 10, Sequence 3, P Sequence 7, P Sequence 7, P

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Run

Sequence:

Minimum DB Maximum DB

Database

Result Š.

Searched:

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Score 42.6; DB 2;
Pred. No. 3.1e-07;
1; Mismatches 5;
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Computable
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,461
FILING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            PROSTATE CANCER DRUG SCRE
US-08-975-080-35
US-09-630-706-10
US-09-406-610
US-09-406-610
US-09-814-095-7
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US-09-797-906-3
US-09-797-906-3
US-09-797-906-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HENDERSON, Daniel R. APPLICANT: SCHUUR, ETIC R. APPLICANT: LAMPARSKI, Henry G. APPLICANT: YU, DE CHAO TITLE OF INVENTION: PROSTATE CANCEI TITLE OF INVENTION: ENING NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
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APPLICATION NUMBER: 08/906,192
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cacherine, Polizzi M
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/09022461; Patent No. 5964371; GENERAL INFORMATION:
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88.2%;
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TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.2
Matches 45; Conservative
  14796
114796
118739
28720
335060
335060
43050
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62804
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ZIP: 94304-1018
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4035.781 Million cell updates/sec
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Sequence 16, 1
Sequence 15, 1
                                                                                        February 10, 2003, 21:12:29; Search time 3.87546 Seconds
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Sequence 1, A
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Sequence 8, 1
Sequence 6, 1
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Sequence 6,
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Sequence 3,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Compugen Ltd.
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US-08-909-965C-4
US-08-927-165A-5
US-09-484-970B-142
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US-08-147-66-6

US-09-024-472-6

US-09-018-584A-16

US-09-018-584A-15

US-09-185-987-471

US-08-832-883-65
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US-09-749-588-3
US-09-146-053-6
US-09-813-817-3
US-09-978-197-3
US-09-345-882-1
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US-08-832-877-48
PCT-US93-06251-23
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                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-323-873A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-578-649-3
                                                                                                                                                                                                                                  441362 segs, 153338381 residues
             GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
                                                                                                                                US-09-942-310-2_COPY_5_55
51
                                                                                                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12047
12047
16389
17327
36159
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162450
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1699
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3865
3865
11558
12394
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Match 1
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Gaps

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Length 12047; Indels

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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 16389
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Fatent No. 5440739
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Avraham, Shalom
TITLE OF INVENTION: HEMATOPOLETIC C.
TITLE OF INVENTION: TRANSCRIPTIONAL
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                               80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)833-7533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                         44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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                                                                                                                                                                                        Best Local Similarity
                                                                                TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-07-906-871-15/c
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LOCATION:
                                                                                                                        US-09-741-154-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                   Query Match
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APPLICANT: Yu, De Chao
TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001061
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                                 1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows SOFTWARE: Fast-SEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033.556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34802-20010.00
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                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto
                                                                                                                                                        Sequence 3, Application US/09033556 Patent No. 6432700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 3480
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09741154
Patent No. 6437110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.5%;
Best Local Similarity 88.2%;
Matches 45; Conservative
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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LENGTH: 12047 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             ^{\mathsf{C}}
                                                                                                                                     US-09-033-556-3/c
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                                                                                                                    RESULT 2
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HEMATOPOIETIC CELL SPECIFIC TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND USES
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                                                         Gaps
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                                                                                                                                455 TCAAGACCAGCCTGGCCAACATGGCAAAAACCCCGTCTCTACTAAAAATACA 405
Score 41; DB 4; Length 16389;
Pred. No. 1.4e-06;
1; Mismatches 6; Indels
                                                                                                      51
                                                                                                   1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Sterne, Kessler, Goldstein & Fox
1225 Connecticut Avenue, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/07/906,871
FILING DATE: 19920103
CLASSIFICATION: 435
                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION 13-39
PRICE APPLICATION DATA:
APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
FILING DATE: 13-JUL-1989
PRIOR APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-JUL-1989
PRIOR APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-JUL-1989
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT APPLICATION NUMBER: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09978197
Patent No. 6403353
GENERAL INFORMATION:
APPLICANT: TAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1178DIV
CURRENT APPLICATION NUMBER: US/09/978,197
CURRENT PILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-03-22
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                                                                                                          Score 41; DB 4; Length 45546;
Pred. No. 1.8e-06;
1; Mismatches 6; Indels
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86.3%; Pred. No. 1.9e-06;
1ive 1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 4; Length 590
Pred. No. 1.9e-06;
1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/09813817; Patent No. 6340583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.4%;
                                                                                                        y Match
Local Similarity 86.3%;
hes 44; Conservative
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SOFTWARE: FastSEQ for Window.
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Best Local Similarity 86.35
Matches 44; Conservative
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nes 44; Conservative
                                               ; ORGANISM: Homo sapiens
US-09-146-053-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
        LENGTH: 45546
                                                                                                                                                                                                                                                                                                                       US-09-813-817-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 59065
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LENGTH: 59065
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                                                                                                               Query Match
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Matches
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APPLICANT: CHANDRAMOULISWARAN, ISHWAT et al
APPLICANT: CHANDRAMOULISWARAN, ISHWAT et al
TITLE OF INVENTION: ASID MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ALED WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOLIGG
CURRENT APPLICATION NUMBER: US/09/749,588
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 4
SCURRENT FILING DATE: Alows Version 4.0
SEQ ID NO 3:
LENGTH: 36159
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86.3%; Pred. No. 1.7e-06;
tive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                             Ouery Match

80.4%; Score 41; DB 1; Le
Best Local Similarity 86.3%; Pred. No. 1.4e-06;
Matches 44; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ryan, James W.
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Vencma, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MGG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09146053A Patent No. 6399349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09749588
Patent No. 6423521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(36159)
; OTHER INFORMATION: D = A,T,C or
US-09-749-588-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.3%
Matches 44; Conservative
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16397..17327
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9745..16396
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9597..9744
                       intron
754..9596
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FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                ; LOCATION:
US-07-906-871-15
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US-09-146-053-6
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OTHER INFORMATION: 5-135-357
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                                                                                               LOCATION: 134134
OTHER INFORMATION:
                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION:
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LOCATION: 146345
OTHER INFORMATION:
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LOCATION: 150329
OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 108471
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                                Sequence 1, Application US/09345882

| Patent No. 6399373
| Patent Newmann.
| Patent Newmann.
| Patent Newmann.
| TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
| TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
| PATENT PAPLICATION NUMBER: US 60/091,315
| PRIOR FILING DATE: 1998-06-30
| PRIOR FILING DATE: 1998-12-10
| PRIOR FILING DATE: 1998-12-10
| NUMBER OF SEQ ID NOS: 140
| SOFTHARE PATENT NOS: 140
| SOFTHARE: PATENT NOS: 140
| SEQ ID NO 1
| LENGTH: 162450
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OTHER INFORMATION: 99-1437-325
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NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198
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OTHER INFORMATION: 5-124-273
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FEATURE:
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                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 106940
OTHER INFORMATION:
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LOCATION: 108106
OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 99098
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LOCATION: 103806
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LOCATION: 108308
                      US-09-345-882-1
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325
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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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.CON: 72771...72817
INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ
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OTHER INFORMATION: polymorphic fragment 5-128-60
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5-136-174
                                                                                                          LOCATION: 134362
OTHER INFORMATION: 5-140-348
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OTHER INFORMATION: 5-148-352
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Sequence 6, Application US/08741406
Patent No. 5721118
Fatent No. 5721118
Fatent No. 5721118
FAPPLICANT: Scheffler, Immo E. TITLE OF INVENTION: Mammalian Artificial Chromosomes and TITLE OF INVENTION: Methods of Using Same NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diago
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 39.4; DB 1; Length 282; 84.3%; Pred. No. 1.9e-06;
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                                                                                                                                                                                                                                                           COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,629
FLING DATE: 07-0CT-1993
CLASSIFICATION: 435
ATTON NUMBER: 35
ATTON NUMBER: 36
REGISTRATION NUMBER: 36
REGISTRATION NUMBER: 36
Housman, David E. FONTION OF NUCLEIC ACIDS
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                                                                                                  Wolf, Greenfield & Sacks, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: M0828/7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/550,717
FILING DATE: 31-CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/741,406
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                                                                                             ADDRESSEE: Wolf, Greentield
STREET: 600 Atlantic Avenue
CITY: Boston
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TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 8:
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LENGTH: 282 base pairs
TYPE: nucleic adid
STRANDEDNESS: single
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: United States
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Matches 43; Conservative
                      TITLE OF INVENTION: AMINUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                               CITY: Boston
STATE: Massachusetts
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MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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US-08-133-629-8
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US-08-741-406-6
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LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                             LOCATION: 97130..97177
OTHER INFORMATION: Polymorphic fragment 5-129-144 SEQ ID33
                                                                                                                                          LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
                                                                                                                                                                                                                                                                                                                                    LOCATION: 99075..99121
OTHER INFORMATION: Polymorphic fragment 5-130-257 SEQ ID55
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OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
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OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
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OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
                                                                                                                                                                                                                                                                     SEQ ID34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.4%; Score 41; DB 4; Le Best Local Similarity 86.3%; Pred. No. 2.5e-06; Matches 44; Conservative 1; Mismatches 6;
                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: POlymorphic fragment 5-130-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-133-629-8; Sequence 8, Application US/08133629; Patent No. 5597694; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Munroe, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .108177
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LOCATION: 108127.
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LOCATION: 108127.
                                                                                                                   NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                             77.3%; Score 39.4; DB 1; Length 327; 84.3%; Pred. No. 2e-06; Live 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             171 TCGAGACCAGCCTGGCCAACTTGGTGAAACCCTGTCTACTAAAAATACA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.4; DB 3; Length 327;
Pred. No. 2e-06;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTTCTACAAAAATACA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mammalian Artificial Chromosomes and TITLE OF INVENTION: Methods of Using Same NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4730 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
NAME: Campbell, Cathryn A.
REGISTRATION UNDHER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2317
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REERENCE/CDCKET NUMBER: P-UD 2317
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/741,406
FILING DATE:
APPLICATION NUMBER: US 08/550,717
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/024,472 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09024472
Patent No. 6133503
GENERAL INFORMATION:
APPLICANT: Scheffler, Immo E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.3%;
Best Local Similarity 84.3%;
Matches 43; Conservative
                                                                                                                                                                             LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 84.3
Matches 43; Conservative
                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-741-406-6
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1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA 51

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                                                                                                                                                   IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jeffery W.
MATERIALS AND METHODS FOR
IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
1 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.3%; Score 39.4; DB 4; Best Local Similarity 84.3%; Pred. No. 2.1e-06; Matches 43; Conservative 1; Mismatches 7;
                                                                                                            Jeffery W. MATERIALS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDUM TYPE: Dischette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16026.9180
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-Feb-1998
CLASIFICATION:
               US-09-018-584A-16; Sequence 16, Application US/09018584A; Patent No. 6238863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 15, Application US/09018584A; Patent No. 6238863; GENERAL INFORMATION: APPLICANT: Schumm, James W.; APPLICANT: Bacher, Jeffery W.
                                                                                                                                                                                                                                Promega Corporation
                                                                                                                                                                                                                                              2800 Woods Hollow Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pGem3Zf(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16C
TELECOMMUNICATION INFORMATION:
                                                                    GENERAL INFORMATION:
APPLICANT: Schumm, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MAPERIALS
TITLE OF INVENTION: IDENTIFYI
TITLE OF INVENTION: REPEAT DN
NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSITION IN GENOME:
CHROMOSOME/SEGMENT: 8 qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (608) 257-3501
TELEPAX: (608) 257-2275
INFORMATION FOR SEQ ID No: 16
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Genomic DNA HYPOTHETICAL; no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circular
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                                                                                                                                                                                                                                                                                     Wisconsin
                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 53711-5399
                                                                                                                                                                                                                                                                    Madison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G153
                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-018-584A-15
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RESULT 13
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Batent No. 626234

GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER PILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-031
NUMBER OF SEQ ID NOS: 544

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 488
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                 ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
CITY: Madison
STATE: Wisconsin
COUNTRY: U.S.A.
2.1P: 53711-539
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
APPLICATION DATA:
APPLICATION UNMBER: US/09/018,584A
FILING DATE: 04-Feb-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION UNBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELEPHONE: (608) 257-2501
TELEPHONE: (608) 257-2525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHRACTERISTICS:
LENGTH: 372 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: plasmid, pGem3ZE(+); CLONE: G152; POSITION IN GENOME: CHROMOSOME/SEGMENT: 8 qter US-09-018-584A-15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(488)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
LIBRARY: plasm
CLONE: G152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-385-982-471/C
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                                                                                                                                                                                                                                    Search completed: February 11, 2003, 05:41:33 Job time : 43.8755 secs
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-471
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2467, Ap 4, Appli

Sequence 315, App Sequence 345, App Sequence 1077, App Sequence 1077, App Sequence 1078, Ap Sequence 3445, Ap Sequence 2292, Ap Sequence 2292, Ap Sequence 602, App Sequence 601, App Sequence 601, App Sequence 251, App Sequence 251, App Sequence 255, App Sequence 250, App

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Length 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.5%; Score 42.6; DB 9; Length 4
88.2%; Pred. No. 3.2e-07;
Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCAAGACCAGCCTGGACAACTTGGAAGAACCSGGTCTCTACAAAAAATACA
              US-09-893-348-4
US-09-822-849A-418
US-09-876-889-355
US-09-764-847-1077
US-09-764-847-1077
US-09-764-847-1077
US-09-764-84-1079
US-09-764-84-1079
US-09-764-84-1079
US-09-764-869-2292
US-09-764-869-1657
US-09-764-869-1657
US-09-764-869-1657
US-09-764-869-1657
US-09-764-869-1657
US-09-764-869-1657
US-09-764-870-602
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US-09-764-869-1791
US-09-880-107-2362
US-09-764-847-1280
US-09-764-860-990
                                                                                                                                                                                                                                                                                                                                       US-09-860-670-251
US-09-860-670-249
US-09-860-670-252
US-09-860-670-253
US-09-860-670-253
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Patent No. US20020165144a1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
NUMBER OF SEQ ID NOS: 1531
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Patent No. US20020045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gilcher, Jeffrey R.
IIILE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
  Query Match 83.55
Best Local Similarity 88.23
Matches 45; Conservative
                                        2446
4978
6371
6640
8369
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9558
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14448
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15046
15849
17335
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11869
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13996
14001
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; ORGANISM: Homo sapiens
US-09-946-807-952
                                                                                     US-09-946-807-952/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-795-668-952/c
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Sequence 952, App
Sequence 952, App
Sequence 1903, Ap
Sequence 1903, Ap
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 855, Ap
Sequence 22, Appli
Sequence 825, Ap
Sequence 825, Ap
Sequence 826, Ap
Sequence 826, Ap
Sequence 826, Ap
Sequence 826, Ap
                                                                                                                                                                               (without alignments) 5222.300 Million cell updates/sec
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                                                                                                                                                     February 11, 2003, 03:31:30 ; Search time 4.62902 Seconds
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/cgn2_6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptcdata/2/pubpna/NCSO8_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/USO9_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-764-869-1902

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10 US-09-804-471A-3

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Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM nucleic - nucleic search, using sw model
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seq length: 2000000000
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Best Local Similarity 88.2
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                   Length 401;
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
                                                                                                                                                                                                                                                                                                                                                                                         84 TCAAGACCAGCCTGGGCAACATGGAAAAACCCTGTCTTACCAAAAATACA 34
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Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
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Pred. No. 3.2e-07;
1; Mismatches 5;
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APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 952
LENGTH: 401
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 952
LENGTH: 401
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Best Local Similarity 88.2%;
Matches 45; Conservative
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SEQ ID NO 1902
LENGTH: 4962
                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-795-668-952
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US-09-795-686-952/c
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GENERAL INFORMATION:
APPLICANT: Yu, De Chao
APPLICANT: Sequesial 
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88.2%; Pred. No. 8.1e-07;
Live 1; Mismatches 5; Indels 0;
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TITLE REFERENCE PEOOT Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE PEOOT
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEO ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
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6.4e-07;
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Pred. No. 6.4e-07;
1; Mismatches
                                  88.2%; Pred. No. 6.46
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Best Local Similarity 88.2%;
Matches 45; Conservative
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US-09-764-869-1903
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Matches 45; Conserv
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US-09-764-869-1903
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US-09-875-228-1/c
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Sequence 3, Application US/10238709

Publication No. US20030022340A1

GENERAL INFORMATION:
APPLICAMY: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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Patent No. US2002013232A1

GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: US/09/804,471A
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT PILLICA DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 1.5e-06;
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88.2%; Pred. No. 1.7e-06;
iive 1; Mismatches 5;
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                                 NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3
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                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(116592)
OTHER INFORMATION: n = A,T,C or
            2001-03-28
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88.2%;
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Matches 45; Conservative
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Matches 45; Conservative
            CURRENT FILING DATE:
                                                                                                                                                      ORGANISM: Human
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ORGANISM: Human
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LENGTH: 174493
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LENGTH: 174493
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US-10-238-709-3/c
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                                                                                                                                  TYPE: DNA
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APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
APPLICANT: Schuur, E.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE TITLE OF INVENTION: BINANCER AND METHODS OF USE THEREOF
FILE REFERENCE: 348022000900
CURRENT APPLICATION NUMBER: US/09/875,228
CURRENT FILING DATE: 1998-03
PRIOR FILING DATE: 1998-03
PRIOR FILING DATE: 1998-03-02
PRIOR SEQ ID NOS: 38
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Patcht No. US20020142416A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPERBNCE: CL001192
CURRENT APPLICATION NUMBER: US/09/818,512
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Pred. No. 8.1e-07;
1; Mismatches 5;
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Fatent No. US20020102731A1
GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, 21v
APPLICANT: Sandalon, 21v
APPLICANT: Gatenko, Dmitri
TILE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : PatentIn version 3.0
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Best Local Similarity 88.2%;
Matches 45; Conservative
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SEQ ID NO 1
LENGTH: 12047
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CRGANISM: Homo sapiens
US-09-782-378A-17
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SEQ ID NO 17
LENGTH: 56737
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US-09-875-228-1
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA128
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/908,711
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PRIOR PRILING DATE: 2001-07-70
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01
                              ; Sequence 22, Application US/09908711; Patent No. US20020045230A1
                                                                        GENERAL INFORMATION:
       US-09-908-711-22/c
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Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBENC: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1636
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                                                                                                              Score 42.6; DB 10;
Pred. No. 1.7e-06;
1; Mismatches 5;
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88.2%; Pred. No. 1.4e-06;
tive 0; Mismatches 6;
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Pred. No. 1.1e-06;
1; Mismatches 6;
; NAME/KEY: misc_feature; LCATION: (1)...(174493); OTHER INFORMATION: n = A,T,C or G US-09-804-471A-3
                                                                                                                83.5%;
88.2%;
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Matches 45; Conservative
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Best Local Similarity 88.2°
Matches 45; Conservative
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Matches 44; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapien
US-09-867-701-8259
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| Sequence 822. Application US/09867701
| GENERAL INFORMATION:
| APPLICANT: Aglate, Paul A. |
| APPLICANT: Adlate, Paul A. |
| APPLICANT: Adlate, Paul A. |
| APPLICANT: Harlocker, Susan L. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER |
| CURRENT APPLICATION NUMBER: US/09/867,701 |
| CURRENT FILING DATE: 2001-05-29 |
| NUMBER OF SEQ ID NOS: 10912 |
| SEQ ID NO 8232 |
| LENGTH: 419
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PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: USO1/01312
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-31
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR PILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR PILING DATE: 2000-06-07
SEQ ID NO.S: 167
SEQ ID NO.S: 167
SEQ ID NO.S: 187
CORGANISM: Homo sapiens
PEATURE:
COCATION: (138)
OTHER INFORMATION: n equals a, L, g, Or C
US-09-908-711-22
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; ORGANISM: Homo sapien
US-09-867-701-8232
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US-09-867-701-8232/c
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Novel human prostate cxp
Human prostate cxp
Human prostate cxp
Human prostate cxp

prostate exp human polynu prostate exp prostate exp

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Human 1mmune/hacma

Human immune/haema Human immune/haema

Human immunc/hacma Human immunc/hacma Human breast cance Human breast cance Human breast cance Human breast cance Human breast cance

Human prostate exp N. meningitidis pa Human nervous syst

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Cytochrome P450; CYP2D6; promoter; drug metabolism; human; diagnosis; therapy; ds.
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/*tag:- a
/note:- "amplification primer upf14"
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/note "sequencing primer R2"
complement (565..577)
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/note~ "sequencing primer R3"
complement (968..988)
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/note= "sequencing primer F2"
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/note= "sequence primer R1"
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AAK80193
AAZ93705
AAK79153
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AAK70625
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ABV58508
AAA81674
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ABN63715
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ABL62279
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ABV55775
AAF65385
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  (first entry)
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Human reproductive
Human musculoskele
Human osteoblast d
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Human cytochrome P
Human CYP2D6 gene
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                                                                              February 10, 2003, 20:43:59; Search time 16.6596 Seconds (without alignments) 5542.256 Million cell updates/sec
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                           nucleic search, using sw model
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AAH26179
AAD34214
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ABL66777
AAL37445
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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; 0

Length 1669;

Score 40.6; DB 22; Pred. No. 3.2e-06;

Query Match Best Local Similarity

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cargets of the CYP2D6 gene product.
/*tag=
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                                                       Raimundo S, Zanger U;
                                                           WPI; 2001-457734/49.
                                   WO200155432-A2
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                primer_bind
                                       02-AUG-2001
                      5'UTR
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1605..1623
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note= "sequencing primer R5"
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.620..1669
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The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene. The promoter region was amplified by PCR from leucocyte DNA of over 50 individuals, and sequenced.

8 Previously unknown single nucleotide polymorphisms (SNP) were care identified. These were at: base 36 (base -1584 according to the identified. These were at: base 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature), where the SNP was C to G, occurring at an estimated frequency of approximately 20% in the position 194 (-1426), C to T, approximately 20% frequency, neutral function; position 620 (-1000), G to A, approximately 20% frequency, neutral function; position 620 (-1000), G to A, approximately 30% frequency, unknown function; position 940 (-680), C to T, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 950 (-1000), C to T, approximately 30% frequency, unknown function; position 940 (-200), C to T, approximately 30% frequency, unknown function; position 940 (-200), C to T, approximately 30% frequency, unknown function; 1255 (-365), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function; position 940 (-680), C to A, approximately 30% frequency, unknown function and 1258 (-325).

The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates anti-darressant solority for clearance of CYP2D6 Substrates anti-darressant solority is receptor; inhibitor maniforming the position of CYP2D6 substrates anti-darressant solority is receptor anti-darressant solority is receptor anti-dar polynucleotide capable of hybridizing to CYP2D6 promoter useful for the optimization of drug therapies using substrates of cytochrome P-450 correlation between genotype and phenotype in the CYP2D6 polymorphism. Testing for the mutation will allow the identification of intermediate metabolizers and therefore allow quantitative predictions to be made on in vivo drug metabolism capacity, thus providing a very potent tool for improving the therapy of diseases with drugs that are antidepressant, selective serotonin reuptake inhibitor, incuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP2D6 promoter. The strong association of the common C to G mutation at -1584 bp with increased enzyme activity significantly improves the Claim 1; Fig 1; 41pp; English.

Sequence 1669 BP; 413 A; 376 C; 534 G; 338 T; 8 other;

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polynucleotide capable of hybridizing to CYP2D6 promoter useful for ne optimization of drug therapies using substrates of cytochrome P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene, which includes G at position 36 (base -1584 according to the Human Cytochrome P450 Allale Nomenclature). The presence of C at position -1584 bp is a marker for low enzyme activity, whereas there is strong association of G at position -1584 bp with increased enzyme activity. The C to G single nuclectide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of C CYP2D6 substrates (antiarrhythmic, beta-adrenergic receptor antagonist, tricyclic antidepressant, selective servoin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP2D6 promoter. The novel variant forms of the development of a pharmacodynamic profile of drugs for a given caption, and diagnostic tests for the discrimination of
                                          Gaps
                                                                                                                                                                                                                                                                  Human cytochrome P450 CYP2D6 gene promoter (G mutation at -1584 bp).
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                                                                                                                                                                                                                                                                                              Cytochrome P450; CYP2D6; promoter; drug metabolism; human; diagnosis; therapy; single nucleotide polymorphism; ds.
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                                          Indels
                                                                                     175 CCTATCTCTACTGAAAATAYAAAAGCTAGACGTGGTGGCA 215
                                                                   1 CCTATCTCTACTGAAATAYAAAAAGCTAGACGTGGTGGCA 41
99.0%; Scor.
100.0%; Pred. No. 5.-
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1532..1619
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ligase-based sequenced determination; drug metabolism; chromosome 22;
gene; polymorphism; ds.
                                                                                                                       Gaps
different alleles in human individuals, provide a very potent tool for improving the therapy of diseases with drugs that are targets of the CYP2D6 gene production, and whose metabolism is therefore dependent on CYP2D6 activity.

Once: The present sequence is not shown in the specification but inderived from the CYP2D6 promoter sequence given in the Sequence Listing (see AAH26169).
                                                                                                                                                                                                                                                                   Human CYP2D6 gene 5' flanking region containing polymorphic sites.
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                                                                                                 Length 1669;
                                                                                                                     Indels
                                                                              Sequence 1669 BP; 413 A; 376 C; 535 G; 338 T; 7 other;
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                                                                                               Score 40.6; DB 22;
Pred. No. 3.2e-06;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.2
Matches 41; Conservative 0; Mismatches
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"Polymorphic site"
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'note= "Polymorphic site"
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New sequence determination oligonucleotides, useful for detecting

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detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenoblotics. Human CYP2D6 gene is located on chromosome 22.

The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human CYP2D6 gene 5' flanking region containing polymorphic sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic; ligase-based sequenced determination; drug metabolism; chromosome 22;
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                                                                                                                                                     The invention relates to sequence determination oligonucleotides for
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polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40.6; DB 24; Length 1680; Pred. No. 3.2e-06;
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                                                                                                     Claim 1; Fig 2; 63pp; English.
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21-SEP-2000;
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02-OCT-2000;
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02-OCT-2000;
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    0;
hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human
                                                                                                Gaps
                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19551.
                                                                                                ;
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                                                                                                                             1 CCTATCTCTACTGAAATAYAAAAGCTAGACGTGGTGGCA 41
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                                                                                                                                                                                                                                                                                                                                  WO200157182-A2
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18 - AUG - 2000;
22 - AUG - 2000;
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23-AUG-2000;
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                                CYP2D6 gene.
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Aminoacylase-1; ACY-1; metalloprotein; cytosolic enzyme; human; gene; cytostatic; therapeutic; cancer therapy; ds.
                                                      Genomic DNA of an enzyme similar to human aminoacylase-1 (ACY-1).
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                           10-SEP-2002 (first entry)
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                                                                                                                                                   Key
 ANK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient, s genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cuplynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
co AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis .
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ABL60777/c
ID ABL60777 standard; DNA; 9704 BP.
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2000US-0251988
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule encoding enzymes similar to human aminoacylase-1 (ACY-1) (EC 3.5.1.14) (a metalloprotein Cytosolic enzyme). The ACY-1 similar polynucleotide and encoded peptide sequences can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic agents, and serve as targets for the development of human therapeutic agents that modulate enzyme activity in cells and tissues that express the enzyme. ACY-1 has been found to be expressed in humans in the placenta, T cells from T cell leukemia, ovary, brain, lung and leukocyte, and therefore may be a drug target for cancer therapy and act as a diagnostic marker for these cancers. The present sequence represents the genomic DNA of the enzyme similar to human aminoacylase-1 (ACY-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding enzymes similar to human aminoacylase-1, useful as a drug target and diagnostic marker for cancers e.g. T cell leukemias and ovary, brain or lung cancers -
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 /*tag= u
/number= "10"
7033..7112
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/number= "11"
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7113..7274
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/number= "12"
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P-PSDB; ABB08102.
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AAL05137/c
                                       exon
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THE HERETER REPRESENTATION OF THE PROPERTY OF 
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17 - NOV - 2000; 20000S - 0249212.

17 - NOV - 2000; 20000S - 0249213.

17 - NOV - 2000; 20000S - 0249214.

17 - NOV - 2000; 20000S - 0249215.

17 - NOV - 2000; 20000S - 0249215.

17 - NOV - 2000; 20000S - 0249217.

17 - NOV - 2000; 20000S - 0249245.

17 - NOV - 2000; 20000S - 0249245.

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17 - NOV - 2000; 20000S - 0249264.

17 - NOV - 2000; 20000S - 0249264.
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2000US-0254097
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20 - SEP - 2
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01-DEC-2000;
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11-DEC-2000;
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                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigons. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                           Isolated nucleic acid molecule encoding a reproductive system antiqun is used in preventing, treating or ameliorating a medical condition \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human musculoskeletal system related polynucleotide SEQ ID NO 3810
                                                                                                                                                                            Disclosure; SEQ ID NO 7825; 1297pp + Sequence Listing; English.
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                                                              Barash SC, Ruben SM;
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24-FEB-2000; 20000S-0184664.
26-MAR-2000; 20000S-0184564.
16-MAR-2000; 20000S-0189376.
11-MAR-2000; 20000S-0199874.
18-APR-2000; 20000S-0199123.
19-MAY-2000; 20000S-029467.
20-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0214886.
31-JUL-2000; 2000US-0214887.
31-JUL-2000; 2000US-0216880.
31-JUL-2000; 2000US-021890.
326-JUL-2000; 2000US-021890.
                              (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678
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Best Local Similarity 82.9
Matches 34; Conservative
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08 - NOV - 2000; 2000US - 0246477.
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08 - NOV - 2000; 2000US - 0246611.
08 - NOV - 2000; 2000US - 0246611.
08 - NOV - 2000; 2000US - 024920.
17 - NOV - 2000; 2000US - 0249211.
17 - NOV - 2000; 2000US - 0249214.
17 - NOV - 2000; 2000US - 0249218.
17 - NOV - 2000; 2000US - 0249218.
17 - NOV - 2000; 2000US - 0249245.
17 - NOV - 2000; 2000US - 0249264.
17 - NOV - 2000; 2000US - 0249284.
17 - NOV - 2000; 2000US - 0249284.
17 - NOV - 2000; 2000US - 02492897.
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2000US-0251988.
2000US-0256719.
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451937/48

and/ or prognosing Isolated polypeptide for treating, preventing and/ or prognosin disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Example 2; SEQ ID NO 3810; 781pp + Sequence Listing; English

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, castrointestinal tract, luyer, lung, or urogenital; (b) immune conterned discorders e.g. Addison's discase, allegies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhemmatoid arthritis and ulcerative colitis; (c) cardiovascular disorders e.g. cerebral anoxia and epilepsy;

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at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoporosis or male osteoporosis, osteopora, osteodystrophy, drug-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated colvm marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis, glucocorticoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosing
           parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to genes and their expression profiles are used
                                                                                                                                                                                                                                                                                                                                                               osteoblast; stem cell differentiation; bone tissue deposition;
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                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor stem cell differentiation into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (a) screening modulators of precursor stem cell differentiation introsteoblasts, or bone tissue deposition;
(b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houghton A;
(f) infectious diseases such as viral, bacterial, fungal and
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0
                                                                                                       Length 31730;
                                                                            Sequence 31730 BP; 10793 A; 6331 C; 5682 G; 8924 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    Human osteoblast differentiation related cDNA SEQ ID NO 71.
                                                                                                                                  Indels
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                                                                                                       Score 31; DB 22
Pred. No. 0.031;
                                                                                                                                1; Mismatches
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                                                                                                       Query Match
Best Local Similarity 82.9%;
Matches 34; Conservative
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(PROC ) PROCTER & GAMBLE CO.
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                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J1 D,
and
                                                                                                                                                                                                                            RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
Sequence 86080 BP; 21583 A; 21475 C; 21694 G; 21328 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA differentially expressed in granulocytic cells #132.
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                                                                             DB 24; Length 86080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    granulocytic cell; DNA chip; bacterial infection;
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                                                                                                                                                           6; Indels
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                                                                                                                                                                                                                                                                                                                   Db 38218 CCCATCTCTACTAAAATACAATTAGCTGGGCGTGGTGGCA 38258
                                                                                                                                                                                                                                         1 CCTATCTCTACTGAAAATAYAAAAGCTAGACGTGGTGGCA 41
                                                                                                                       0.037;
                                                                         Score 31; DB 2; Pred. No. 0.037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 132; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK83561 standard; cDNA; 86080
                                                                             75.6%;
82.9%;
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                                                             Query Match
Best Local Similarity 82.9°
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-435328/46.
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27-SEP-2000; 2000US-235863P.
28-SEP-2000; 2000US-236028P.
28-SEP-2000; 2000US-236032P.
28-SEP-2000; 2000US-236033P.
28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236110P.
29-SEP-2000; 2000US-236110P.
29-SEP-2000; 2000US-236110P.
29-SEP-2000; 2000US-236110P.
29-SEP-2000; 2000US-2361173P.
02-OCT-2000; 2000US-237294P.
02-OCT-2000; 2000US-237294P.
03-OCT-2000; 2000US-237396P.
03-OCT-2000; 2000US-237696P.
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                                                                                                                                                                                                                                                                                                           (AVAL-) AVALON PHARM.
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                                                                                                                                                                                                                                                                                                                                      Young PE,
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ABL67239/C
ID ABL672:
XX
AC ABL672:
DT 15-MAY
XX
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     δλ
          from Gs in the tissue. Mi is useful for expression of years(s) and the tissue. Mi is useful for modulating GA, M3 is useful for screening an agent capable of modulating GA, M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, ungal infection and M5 is useful for treating one of the above conditions. The present squence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WHPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                            Gaps
     inflammation with an agent that modulates the expression of gene(s)
                                                                                                                                                                                                                                                       Sequence 86080 BP; 21583 A; 21475 C; 21694 G; 21328 T; 0 other;
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tive 1; Mismatches 6; Indels 0
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                                                                                                                                                                                                                              tp.wipo.int/pub/published_pct_sequences.
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2000US-234923P.
2000US-234924P.
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20-SEP-2000;
20-SEP-2000;
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22-SEP-2000;
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27-SEP-2000;
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                                                                                                                                                                        Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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                                                                                                                                                                        Endress G,
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                                                                                                                                                                        Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 2740; 44pp; English
                                                                                                                                                                    Carter KC,
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01-NOV-2000; 2000US-245084P
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02-AUG-2001
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  Human: cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scroening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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  Thyroid cancer related gene sequence SEQ ID NO:5576.
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2000US-235280P.
2000US-235637P.
2000US-235638P.
2000US-235711P.
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2000US-236032P.
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2000US-236034P.
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2000US-234509P.
2000US-234567P.
2000US-234923P.
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2000US-236842P.
2000US-236891P.
2000US-237172P.
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2000US-234009P
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2000US-237278P.
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25-SEP-2000;
25-SEP-2000;
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26-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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29-SEP-2000;
02-OCT-2000;
                                                                                                                                      Homo sapiens.
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27-SEP-2000;
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28-SEP-2000;
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28-SEP-2000;
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Soppet DR,
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agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma and Wilm's tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reproductive system related antigen; reproductive system disorder; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            Sequence 167343 BP; 49550 A; 37098 C; 35753 G; 44929 T; 13 other;
                                                                                                                                                                                                                                                                                       Score 31; DB 24; Length 167343;
Pred. No. 0.042;
1; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human reproductive system related antigen DNA SEQ ID NO: 8680.
                                                                                                                                                                                                                                                                                                                                                                            Db 134985 CCTGTCTCTACTAAAAATACAAAAAATTAGGCGTAGTGGCA 134945
                                                                                                                                                                                                                                                                                                                                                           1 CCTATCTCTACTGAAAATAYAAAAAGCTAGACGTGGTGGCA 41
                                                                                                                                                                                                                                                                                          75.6%;
82.9%;
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2000US-0209467.
2000US-0214886.
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2000US-0180628.
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2000US-0218290.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0225266.
2000US-0225267.
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2000US-0189874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 82.9
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200155320-A2
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11-JUL-2000; 2
11-JUL-2000; 2
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14-AUG-2000;
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2000US-0230438.
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2000US-0226279.
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2000US-0236370.
2000US-0236802.
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2000US-0237039.
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2000US-0241787.
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22-AUG-2000;
30-AUG-2000;
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01-SEP-2000;
06-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
01-NOV-2000;
08-NOV-2000;
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26-SEP-2000;
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02-OCT-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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    2000US - 0246528.
2000US - 0246532.
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2000US - 0246611.
2000US - 0246611.
2000US - 0249208.
2000US - 0249211.
2000US - 0249211.
2000US - 0249214.
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2000US-0249299.
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2000US-0250160.
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2000US-0251030.
2000US-0251988.
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2000US-0251479
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08-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 217-NOV-2000; 208-DEC-2000; 208
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Local Sim.
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20000S-0234998
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20 - C
    Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; ene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
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                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin; signal transduction pathway protein; cancer; ds; antisense therapy; gene therapy; neurological disorder; renal disorder; cardiovascular disorder; gastrointestinal disorder; pulmonary disorder; reproductive disorder; immune system disorder; proliferative disorder;
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Sequences AAS28878-AAS28926 represent genomic DNA molecules which encode the immunoglobulin polypeptides of the invention. The polynucleotides and polypeptides can be used to diagnose a pathological condition or a susceptibility to a pathological condition in a subject by determining the presence or absence of a mutation in a DNA sequence or determining the presence or amount of expression of the protein. Alternatively the identification of a binding partner to a sequence allows determination of changes in protein activity. The sequences can be used as research tools for receptors or other signal transduction pathway proteins that interact
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Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C. 3,400 expressed sequence tags identify diversity of transcripts
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Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
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Nat. Genet. 4, 256-267 (1993)
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AQ428360 CITBI-EI-
AA72119 ai40c06.s
AG175523 Pan trogl
BQ653382 AGENCOURT
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_gss_mam;*
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Database

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AQ428360 364 bp DNA linear GSS 24-MAR-1999
CITBI-E1-2576K5.TF CITBI-E1 Homo sapiens genomic clone 2576K5, DNA
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AA7721
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                                                                                                                                                                                                                                                                                                                                                                                    Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building Mobulished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
and search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3.21
Class: BAC ends.
                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="sperm"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
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1 (Dases 1 to 484)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tational Carcer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonalc
                                                                                                                                                                                                            Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 364)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 17; Length 364;
Pred. No. 0.0052;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="2576K5"
/clone_lib="CITBI-E1"
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AQ428360.1 GI:4496126
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AA772119.1 GI:2823902
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Best Local Similarity 95.1%;
Matches 39; Conservative
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Other_GSSs: CTRBI-E2-2576P11.TR

Contact: Shaying Zabo, William Nierman, Mark Adams

Contact: Shaying Zabo, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Fax: 301 838 0208

Email: hbeetigr.corg

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.corg/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: MJ-21

Class: BAC ends.
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Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
                  /clone="HFBDX16"
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/note="Vector: LambdaZaP-II; JT-18 wk gestation, female;
oligo-dT + random primed cDNA synthesis; lambdaZaP-II
vector, 1.0kb average inser size."

a 101 c 90 g 111 t 4 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
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Pred. No. 0.0015;
1; Mismatches (
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/note="Vector: pBeloBAC11;
calTech Human BAC Library I
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
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                                                                                                                                                                                                                                                              99.0%;
ilarity 97.6%;
Conservative
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AQ424894
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Best Local Similarity
Matches 40; Conserv
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AQ428360
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

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Sequencing: TJ
LIBRARY
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BQ653382
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/lange/lange.html
Insert Length: 705 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTT3'], doubte-stranded cDNA was size selected, ligated to ECo RI adapters (pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento saces and M.Fatima Bonaldo. RNA from spotsatic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Totoki, Y., Watanabe, H. and Sakaki, Y. Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission Submitted (02-Aug-2001) Asao Fuliyama, The Institute of Physical Submitted (02-Aug-2001) RikEM), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9770) Clones are derived from the chimpanzee BAC Library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                    /clone_lib-"Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host-"DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT/T3D (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: lst strand cDNA was primed with a Not I - oligo(dT)
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Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library RPCI-43
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1359466"
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AG175523.1 GI:16705203
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/organism."Homo sapiens"
/db.xrefe"taxon:9606"
/clone.ib.minAgge:6282557"
/clone_lbe.nim.H.MGC_l00"
/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_hostw.Mpl08 (phage-resistant)"
/lab_hostw.Mpl08 (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally cloned
into BCORI/AnoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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AGENCOURT_8188655 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:6282557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Standford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
165 c 182 g 123 t
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/organism~"Pan troglodytes"
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Location/Qualifiers
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/clone="RP43-046H20.TJ"
                                                                             Location/Qualifiers
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pBACe3.6
EcoRI
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BQ653382
BQ653382.1 GI:21777554
                          ECORI
ECORI
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85.0%;
                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                 34; Conservative
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     Vector
R.Site 1
R.Site 2
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yddf07.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone HGR repetitive element; contains Alu repetitive element; contains T8410.
                                                                        1 (bases 1 to 319)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2255 Col=18 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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Insert Size: 918
High quality sequence stops: 398 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                            High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
721: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2255 row: M column: 18
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Pred. No. 2.2;
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BQ892326
BQ892326.1 GI:22284340
BSFT.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOrgh?; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: pOrgh?; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: porgh?; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: porgh?; Site_1: Colned
/note EcoRI/XhoI sites using the following 5' adaptor:
/note_Organ: Size-selected >500bp for average insert size
/note.library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
// Infer Technologies). Note: this is a NIH_MGC
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319 bp DNA linear GSS 04-AUG-1998
HS_2255_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2255 Col=18 Row=M, DNA sequence.
AQ068839.1 GI:3384038
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MCC clone distribution information can be a sequence of the corporation of through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM2513 row: a column: 23

High quality sequence stop: 244.
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    .1103
    /organism="Homo sapiens"

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/clone="IMAGE:6299806"
/clone_lib="NIH_MGC_100"
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RESULT 8 AQ068839

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TITLE COMMENT

BQ892326

RESULT 7

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Gaps

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Bonaldo, Ph.b.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 673 Std Error: 0.00
                                                                                                                                                                                                                                                                                                      AIG38655 468 bp mRNA linear EST 14-DEC-1999 tt25c03.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2241796 3' similar to dontains Alu repetitive element;contains element PTR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote—"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " all 3 c 129 g 134 t lothers
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Eukaryota; Metazoa; Chordata; Craniata; Vertobrata; Eutoleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Produzement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
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                                                                                    Score 31;
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82.98;
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82.9%;
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Matches 34; Conservative
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1 (buses 1 to 445)
Mahatras, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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/clone="plate=2236 Col=13 Row=p"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:111301"
/clone="lib="soares fetal liver spleen lNFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tal: (206) 616-3618
Fax: (206) 616-3861
Email: jwallace@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 1
Pred. No. 2.2;
  Std Error: 0.00
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                                       High quality sequence stop: 398.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 445.
Location/Qualifiers
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82.9%;
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Insert Length: 918
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Best Local Similarity 82.99
Matches 34; Conservative
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                      Seq primer: T3
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Class: BAC e
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AQ154068
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                                                                 Homo sapiens
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AQ013280/c
LOCUS
                                                             ORGANISM
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TITLE
JOURNAL
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/organism="Homo sapiens"
/db_xref="Robins566398"
/db_xref="Robins566398"
/db_xref="taxon:9606"
/clone="IMAGE:154015"
/clone="IMAGE:154015"
/clone="Image:154015"
/clone="Image:154015"
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/clone="Image:154015"
/clone="Image:154015"
/clone="Image:154015"
/clone="Image:154015"
/dev_stage="adult"
/dev_stage="adul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded CDNA was ligated to ECO RI addrors (Pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 487)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Wohldman,P. and Wilson,R.
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                                                                                            EST 18-MAY-1995
                                                                                         R48796 167 18-MAY-195 PARNA linear EST 18-MAY-195 yj69f04.sl Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154015 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1188
High quality sequence stops: 315 Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1188 Std Error: 0.00
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High quality sequence stop: 315.
Location/Qualifiers
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BF213410
BF213410.1 GI:11106996
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Best Local Similarity
Matches 34; Conserv
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                        RESULT 12
R48796/c
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BF213410
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KEYWORDS
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/issue_type="from acute myelogenous leukemia"
/lab_host="DBIOB (TI phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Site] (ggocgcctcggcc); Site_2: SfII (ggocattatggcc); Site_1: SitI (ggocattatggcc); Site_2: SfII (ggocattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5, and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCANTATGGCC3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGAGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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1 (bases I to 570)
Adams, M. D., Rounsley, S. D., Zhao, S., Field, C. E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. C.
Venter, J. C.
Orber, GSS: RPCIII-23B18.TVB RPCIII-23B18.TPB
Contact: Mark Adams
The Institute for Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ013280 578 bp DNA linear GSS 14-APR-1999
RPCI11-23B18.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23B18,
Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 568)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.e. column: 18
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/db_xref="taxon:9606"
/clone="IMAGE:4070393"
/clone_lib="NIH_MGC_55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 554.
Location/Qualifiers
1. 568
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uppublished
2 (base, 1 to 659)
Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Birect Submission
Chamical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:Bl-45-503-9111, Fax:81-45-603-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG048643.1 GI:16585535
GSS.
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-028112.F.
Pan troglodytes
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Pan.
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Tel: 301 838 0200
Eax: 301 838 0200
Enx: 301 838
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Pan troglodytes DNA, clone: PTB-028112.F, genomic survey sequence.
AG048643
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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/organism="Pan troglodytes"
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/db_xref="GDB: 7508489"
/db_xref="taxon: 9606"
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/clone="lb="RPCI-11"
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/cell_type-"Lymphocytes"
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1. .578
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              /sex="male"
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,223
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US-08-757-223-7/c
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LENGTH: 9704
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TYPE: DNA
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Sequence 59,
Sequence 16,
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Sequence 20,
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US-09-128-155-16
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US-09-128-155-16
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US-09-641-638-376
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US-09-210-748A-3
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      GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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US-09-814-951A-3/C
Sequence 3, Application US/09814951A
SERIE NECENT. SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN AMINOACYLASE, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN AMINOACYLASE, AND USES THEREOF
FILE REFERENCE: CLOO1179
CURRENT APPLICATION NUMBER: US/09/814,951A
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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| Patent No. 6136530
| GENERAL INFORMATION:
| APPLICANT: Podusio, Shirley E. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ASSESSING RISK TITLE OF INVENTION: FACTORS IN ALZHEIMER'S DISEASE
| VORBESPONDENCES: 13 | CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: 2200 Ross Avenue, Suite 2200 | CITY: Dallas
                Sequence 3 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 3 
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85.0%; Pred. No. 0.0014;
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STATE: Texas
ZIP: Texas
ZIP: T5201-6776
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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US-09-797-906-3
US-09-345-882-1
US-09-128-155-17
US-09-128-131-17
US-09-026-033-18
US-09-026-033-23
US-09-026-033-23
US-08-545-860D-63
PCT-US94-04496-63
US-08-545-66
US-08-754-049
US-09-754-250-3
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US-09-131-133A-3
US-09-564-805-217
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61.0 162450
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NAME/KEY: misc_feature
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SEQ ID NO 3
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APPLICANT: LI, Jiayin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLESQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 43950
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APPLICANT: YE, Jane et al.
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOI158
CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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64.9%; Score 26.6; DB 3;
Best Local Similarity 82.9%; Pred. No. 0.11;
Matches 29; Conservative 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 30806 CCTGTCTCTACTGAAAATACAAAAATTAGCCGGG 30772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1296 CCTGTCTCTACTGAAAATACAAAAATTAGCCGGG 1262
FILING DATE: NO. 6136530ember 27, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REFERENCE/DOCKET NUMBER: 4-003US
TELEPHONE: 214/740-8785
TELEPHONE: 214/740-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26.6; DB Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCTATCTCTACTGAAATAYAAAAAGCTAGACGTG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCTATCTCTACTGAAAATAYAAAAAGCTAGACGTG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09735934A Patent No. 6372468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09800960 Patent No. 6387677
                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5375 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.9%;
82.9%;
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Best Local Similarity 82.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-757-223-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-735-934A-3/c
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LENGTH: 62804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-735-934A-3
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US-09-800-960-3
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Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY VENYION: ISOLATED HUMAN PROTEASE PROTEINS, VENYION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND VENYION: USES THERROF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000968
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                              Length 62804;
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                                                                                                                     Indels
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                                                                              DB 4;
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Pred. No. 0.19;
                                                                            Score 26.6; DE Pred. No. 0.18; 1; Mismatches
                                                                                                                                                            1 CCTATCTCTACTGAAAATAYAAAAAGCTAGACGTG 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ISOLATED HUMAN PROPER TITLE OF INVENTION: NUCLEIC ACID MOLECULI TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOO1151CIP CURRENT APPLICATION NUMBER: US/09/797,906 CURRENT FILLING DATE: 2001-03-05 NUMBER OF SEQ ID NOS: 5
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3
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US-09-741-150-3
: Sequence 3, Application US/09741150
: Patent No. 6436689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature; LCCATION: (1)...(112132); OTHER INFORMATION: n = A,T,C or G US-09-741-150-3
                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09797906
Patent No. 6329188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
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; OTHER INFORMATION: n = A,T,C or
US-09-797-906-3
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82.9%;
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82.9%;
                                                                            Query Match
Best Local Similarity 82.9%;
Matches 29; Conservative
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Best Local Similarity 82.9 Matches 29; Conservative
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Best Local Similarity
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APPLICANT: Zianghe
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ORGANISM: Human
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US-09-797-906-3/c
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Gaps

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; NAME/KEY: misc_feature
; LOCATION: (13641)
; OTHER INFORMATION: n = adenosine or guanine or cytosine or thymidine
US-09-608-285A-42
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APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CORRENT APPLICATION NUMBER: 09/583,231
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-04-25
PRIOR PELING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/581,238
PRIOR PELING DATE: 1090-06-05
PRIOR PELING DATE: 1090-06-05
PRIOR PELING DATE: 1999-06-09
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-03-19
PRIOR PELING DATE: 1999-03-19
PRIOR PELING DATE: 1999-03-04
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1998-07-16
PRIOR PELING DATE: 1998-07-16
PRIOR PELING DATE: 1998-07-16
PRIOR PELING DATE: 1998-07-16
PRIOR PELING DATE: 1999-07-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.9%; Score 25.8; DB Best Local Similarity 76.9%; Pred. No. 0.28; Matches 30; Conservative 1; Mismatches
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OTHER INFORMATION: CD39-L4/L66 Gene Sequence
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 42
LENGTH: 14747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 59, Application US/09608285A
; Patent No. 6335013
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NAME/KEY: CDS
LOCATION: (2734)..(2877)
                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (245)..(461)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ford, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-608-285A-59/c
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LENGTH: 15977
                                                                                                                                                                                                                                                             TYPE: DNA
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US/09/608,285A
PRIOR APPLICATION NUMBER: US/57,800
PRIOR PILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 09/587,800
PRIOR PLING DATE: 2000-04-25
PRIOR PAPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,286
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR PILING DATE: 1999-07-09
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GENERAL INFORMATION:
APPLICANT: Ozellus, Laurie J.
APPLICANT: Breakeffeld, Xandra O.
TITLE OF INVENTION: TORSIN, TORSIN GENES, AND METHODS OF USE
FILE REFERENCE: MGH-1184PA2
CURRENT PELLON NUMBER: US/09/218,363
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 09/099,454
EARLIER FILING DATE: 1998-06-18
EARLIER FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASESEQ FOR Windows Version 3.0
LENGTH: 3568
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        Indels
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                                                                                      Db 51462 CCCATCTACTAAAAAATACAAAAAAGTAGCGTG 51496
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                                                         1 CCTATCTCTACTGAAATAYAAAAGCTAGACGTG 35
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Patent No. 6335013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NAME/KEY: CDS | LOCATION: (994)...(1863) | NAME/KEY: misc_feature | LOCATION: (1)...(3568) | COTHER INFORMATION: n ~ A,T,C or G US-09-218-363-3
                                                                                                                                                                                                                    US-09-218-363-3/c
; Sequence 3, Application US/09218363
; Patent No. 6387616
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76.98;
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Best Local Similarity 76.9
Matches 30; Conservative
     Conservative
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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ORGANISM: Homo sapien
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US-09-608-285A-42/C
29;
  Matches
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Patent No. 611/654

GENERAL INFORMATION:
APPLICANT: Pat, Yand
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NUMBER: US/09/128,155

CURRENT APPLICATION NUMBER: US/09/128,155

CURRENT ELING DATE: 1998-08-03

EARLIER FILING DATE: 1998-07-02

EARLIER FILING DATE: 1998-07-02

EARLIER PILING DATE: 1997-08-04

NUMBER: OF SEQ ID NUMBER: US 60/054,646

EARLIER FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEO for Windows Version 3.0 SEQ ID NO 16 LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (15702)..(15839)
MAME/KEY: misc_feature
LOCATION: (14871)
OTHER INFORMATION: n = a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(152331); OTHER INFORMATION: n = A,T,C or G US-09-128-155-16
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Best Local Similarity 76.9
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                       (11613)..(11728)
                                                                                                                                                                                                                                                                                                                                         (13146)..(13691)
                                                                  CDS
(5326)..(5414)
CDS
: (5723)..(5802)
                                                                                                                                                                                             (7758)..(7859)
                                                                                                                                                                                                                                 (8712)..(8852)
                                                                                                                                                                                                                                                                   (9831)..(9887)
CDS
(4364)..(4439)
                                                 (4679)..(4714)
                                                                                                                                           CDS
(6751)..(6812)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-128-155-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-608-285A-59
                                                                                                                                                                                                                                                                                                       LOCATION:
NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME/KEY:
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NAME/KEY:
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NAME/KEY:
LOCATION:
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               LOCATION:
NAME/KEY:
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RESULT 11

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GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEP
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILE OF TEL CATON NUMBER: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                                      Score 25.2; DB Pred. No. 0.66; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.0%; Score 25; DB 4
illarity 80.0%; Pred. No. 0.32;
Conservative 1; Mismatches
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APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LUCATION: (1)...(581); OTHER INFORMATION: n = A,T,C or G US-09-385-982-12
; Sequence 3, Application US/09851896
; Fatent No. 6410325
                                                                                                                                                                                                                                                                                       61.5%;
84.4%;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.44
Matches 27; Conservative
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                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 28; Conserv
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US-09-385-982-12/c
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Indels

Length 1643;

Score 25; DB 4 Pred. No. 0.39;

1; Mismatches

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APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Spauding, Vikii
APPLICANT: Spauding, Vikii
APPLICANT: Spauding, Vikii
APPLICANT: Appeting, Michael J.
TITLE OF INVENTION: ENCODING THEM
MIMBER OF ENCHRONGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                     1 CCTATCTCTACTGAAAATAYAAAAAGCTAGACGTG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                              ; NAME/KEY: CDS
; LOCATION: (70)..(106$)
; OTHER INFORMATION: human cathepsin S
US-09-701-685-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
ATTORNEY-AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 496-8284
TELEFRAX: (617) 476-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09014969
; Patent No. 5965397
                                                                                                                                                                                                              Query Match 61.0%;
Best Local Similarity 80.0%;
Matches 28; Conservàtive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobs, Kenneth
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CORRESPONDENCE ADDRESS:
                          TYPE: DNA ORGANISM: Homo sapiens
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MOLECULE TYPE: CDNA

US-09-014-969-1
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Best Local Similarity
Matches 28; Conserva:
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CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Jacobs
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US-09-014-969-1/C
    LENGTH: 1643
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                                                            TITLE OF INVERTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVERTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEST. 0510-091
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-12
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APPLICANT: Schneider, Patrick
APPLICANT: Yamamoto, Karen K.
APPLICANT: Franch, Cynthia K.
APPLICANT: French, Cynthia K.
APPLICANT: Reprogen, Inc.
TITLE OF INVENTION: Use of Cathepsin S in the Diagnosis and Treatment of
FILE OF INVENTION: Endometriosis
FILE REFERENCE: 018002-001310S/09/701,685
CURRENT APPLICATION NUMBER: US/09/701,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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NAME/KEY: misc_binding
LOCATION: 481..500
COTHER INFORMATION: 12-878-153.misl, potential
NAME/KEY: misc_binding
LOCATION: 502..51
LOCATION: 502..51
COCATION: 349..369
COCATION: 349..369
COCATION: 349..369
COCATION: 389..899
COCATION: 489..513
COCATION: 389..513
COCATION: 389..513
COCATION: 389..533
COCHER INFORMATION: 12-878-153 potential probe
US-09-641-638-376
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Pred. No. 0.35;
1; Mismatches 6; Indels
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PRIOR FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: US 60/088,017
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09701685
Patent No. 6387629
Bougueleret, Lydie
Chumakov, Ilya
Cohen, Annick
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80.0%;
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SOFTWARE: Patent.pm
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Best Local Similarity 80.0
Matches 28; Conservative
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LOCATION: 501
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LENGTH: 1001
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US-09-701-685-1
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Length 2509;
                       Indels
 DB 2;
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                                            1 CCTATCTCTACTGAAAATAYAAAAGCTAGACGTG 35
                      1; Mismatches
 Score 25;
Pred. No. (
61.0%;
80.0%;
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Search completed: February 11, 2003, 05:42:25 Job time : 55.1156 secs

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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 4031
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Sequence 281, App
Sequence 273, App
Sequence 174, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 230, Appli
                                                                                                                                                                     February 11, 2003, 03:31:30 ; Search time 3.72137 Seconds (without alignments) 5222.300 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US07_NW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-764-877-3810

US-09-964-824A-273

US-09-974-298-124

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US-09-764-867-3470

US-09-764-869-2372

US-09-764-867-1579

US-09-918-686-2

US-09-918-686-1

US-09-918-686-1

US-09-918-686-1

US-09-918-686-1

US-09-918-686-1

US-09-918-686-1

US-09-9764-847-12317

US-09-962-436-36

US-09-962-436-36

US-09-962-436-36

US-09-962-436-36

US-09-962-446-1717

US-09-962-446-1717

US-09-962-446-1717

US-09-9764-864-1717

US-09-962-446-1717

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41
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB
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Sequence 3, Application US/10109860
Sequence 3, Application US/10109860
Sequence 3, Application US/10109860
Sequence 3, Application US/20201421a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN AMINOACYLASE, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN AMINOACYLASE, AND USES THEREOF
TITLE OF INVENTION:
CURRENT FILING DATE: 2001/79DTV
CURRENT FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2003-23
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 3
LENGTH: 9704
                                                                                               Sequence 3, Appli
Sequence 314, Appli
Sequence 314, Appli
Sequence 1349, Appli
Sequence 2216, Appli
Sequence 84, Appli
Sequence 1976, Appli
Sequence 1976, Appli
Sequence 1976, Appli
Sequence 2977, Appli
Sequence 2977, Appli
                                   Sequence 217, App
Sequence 17, App1
Sequence 17, App1
Sequence 17, App1
Sequence 3, App11
Sequence 3, App11
 Sequence 862, App
Sequence 2292, Ap
Sequence 415, App
Sequence 456, App
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US-09-967-768A-314
US-09-764-868-1349
US-09-866-670-210
US-09-864-761-2216
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US-09-978-697-84
US-09-978-192A-84
US-09-999-832A-84
US-09-978-189-84
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                                                                     2 US-10-060-332-3
0 US-09-820-003A-3
2 US-10-096-960-3
US-10-243-735-3
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US-09-764-878-224
US-09-801-876B-3
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85.0%; Pred. No. 0.02;
iive 1; Mismatches
                                                                                                                                                                                                                                                       ALIGNMENTS
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US-09-764-877-3810
; Sequence 3810, Application US/09764877
; Patent No. US20020147140A1
 34; Conservative
                           7703
16854
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CORGANISM: Homo sapiens
US-10-109-860-3
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Patent No. US2002014714031

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3470
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Score 31; DB 10; Length 167343;
Pred. No. 0.045;
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                                                                                            Indels
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GENERAL INFORMATION:
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298; CURRENT FILION NUMBER: 00/238,331
PRIOR FILING DATE: 2001-10-04; PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194; SOGTWARE: PERL PROGRAMMARE: PERL PRO
                                                                                                                                                                                                                 Db 134985 CCTGTCTCTACTAAAAAATACAAAAATTAGGCGTAGTGGCA 134945
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80.5%; Pred. No. 0.11;
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; LOCATION: 3880-3917
: OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-124
                75.6%;
82.9%;
                    Query Match 75.65
Eest Local Similarity 82.95
Matches 34; Conservative
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US-09-764-877-3470
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US-09-974-298-124
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APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
FILE REFERENCE: 689290-75
FILE REFERENCE: 689290-75
FILE REFERENCE: 689290-75
FILE REFERENCE: 000-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 281
LENGTH: 167343
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                                                                                                                                                                                                                                                                                      Score 31; DB 10; Length 31730;
Pred. No. 0.037;
1; Mismatches 6; Indels 0
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                                                                                                                                                                                                                                                                                          Query Match 75.6%;
Best Local Similarity 82.9%;
Matches 34; Conservative
                        SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.6
Best Local Similarity 82.9
Matches 34; Conservative
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US-09-962-436-281
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US-09-764-877-3810
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US-09-964-824A-273/C
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US-09-962-436-281/c
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                                                                                                    LENGTH: 31730
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-880-107-3949
SEQ ID NO 1579
LENGTH: 12822
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US-09-918-686-2/c
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LENGTH: 76798
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                                                                                                                                       Query Match
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                                                            GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PRODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001157
CURRENT PAPLICATION NUMBER: US/09/799, 799
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-764-847-1579
Squence 1579, Application US/09764847
Squence 1579, Application US/09764847
Squence 1579, Application US/09764847
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SED ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Rosen et al.
TITLE DO INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.7%; Score 29.4; DB 10;
80.5%; Pred. No. 0.15;
tive 1; Mismatches 7;
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Patent No. US20020061521A1
                                                                                                                                                                                                                                                                                                                                                                                                      : NAME/KEY: misc_feature

: LOCATION: (1)...(88191)

: OTHER INFORMATION: n ~ A,T,C or G

US-09-799-799-3
                     Sequence 3, Application US/09799799 Patent No. US20020132291A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 78.0
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 80.5
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-764-869-2372
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US-09-764-869-2372/C
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                               LENGTH: 88191
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LENGTH: 3941
US-09-799-799-3
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                                                                       67.8%; Score 27.8; DB 10; 78.0%; Pred. No. 0.45;
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                                                                                                                                          1 CCTATCTCTACTGAAAATAYAAAAGCTAGACGTGGTGGCA 41
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                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Proll, Sean
APPLICANT: Paeper, Bryan
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: GENOMIC DELETIONS
TITLE OF INVENTION: GENOMIC DELETIONS
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: 1246, 2572, 2604
; OTHER INFORMATION: n ~ A,T,C or G
US-09-918-686-2
                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/09918686; Patent No. US20020076720A1; GENERAL INFORMATION: APPLICANT: Brunkow, Mary
                                                                                     Best Local Similarity 78.03
Matches 32; Conservative
TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-847-1579
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14619 CCCGTCTCTACTGAAAATACAAAAATTAGCCGGCGTGG 14581
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US-10-025-187-3/c
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; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z84718
US-09-880-107-3949
                                                                                    Length 76798;
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Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCOOS
CURRENT APPLICANTION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                  Indels
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                                                                                                                                                                                              67.8%; Score 27.8; DB 10; 78.0%; Pred. No. 0.56; tive 1; Mismatches 8;
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APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Papeper, Bryan
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: GENOMIC DELETIONS
TITLE OF SEPERATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SEPTIMARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH.: 92139
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LCCATION: 7043, 8369, 8401

CTHER INFORMATION: n = A,T,C or G

US-09-918-886-1
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Patent No. US20020076720A1
                                                                                Query Match
Best Local Similarity 78.0%
Matches 32; Conservative
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US-09-764-877-2317/c
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US-09-918-686-1/c
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LENGTH: 18860
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## Sequence 36, Application US/09962436

| Sequence 36, Application US/09962436
| Patent No. US20020081301A1
| Patent No. US20020081301A1
| APPLICANT: Soppet, Daniel |
| ITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign |
| ITLE OF INVENTION: Sets |

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Sequence 3, Application US/10025187
Fetacht No. US20020159931A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHEFFIELD, VAL
APPLICANT: NISHIMURA, DARRYL
APPLICANT: STONE, EDWARD
TITLE OF INVENTION: A BARDET-BIEDL SUSCEPTIBILITY GENE AND USES THEREOF
FILE REPREBUCE: IONA:034US
CURRENT APPLICATION NUMBER: US/10/025,187
CURRENT FILING DATE: 2001-12-18
PRIOR PRILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATCHTIN VOR: 2.1
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Pred. No. 0.73;
1; Mismatches 7;
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Pred. No. 0.78;
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Job time : 76.7214 secs
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79.5%;
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79.5%;
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-962-436-36
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Best Local Similarity
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Best Local Similarity
Matches 31; Conserv
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US-09-962-436-36/c
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Human nervous syst Human nervous syst Human DNA sequence Rat sequence diffe Drosophila melanog Human cDNA differe

Olfactory receptor Z-chromosomal micr Human prostate exp

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Drosophila melanog Drosophila melanog Drosophila melanog Oligonucleotide fo Oligonucleotide fo Drosophila melanog Human polynucleoti

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Searched:

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Human nervous syst Human nervous syst

Drosophila melanog Human immune/haema luman 1mmune/haema

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Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
ligase-based sequenced determination; drug metabolism; chromosome 22;
gene; polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e
"Polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         b
"Polymorphic site"
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"Polymorphic site"
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"Polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
"Polymorphic site'
                                                                                                                                                                                      AAZ28300
AAZ57791
ABL32506
                                                                                                                                                                                                                                  ABL33236
ABL29030
ABA15397
                                                                     AA293815
AAV48130
                                                                                                                         ABQ15472
ABQ15473
ABL27094
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ABL06992
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ABA15398
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                                                                                                                                                    AAI88442
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                                                                                                                                                                              AAC60025
                                                                                                                                                                                                                  ABK42275
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                                                                                                                                                                                                                                                                                      ABA15399
                                   AAH88704
                                                                                      ABQ89221
                                                                                                                                                                                                                          ABK42274
                                                                                                                                                                                                                                                                                                                  AAK75677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   AAD34214 standard; DNA; 1680 BP
 (first entry)
5884
5884
6281
6286
160755
                                                  2405
149671
144460
285
800
                                                                                              /*tag=
/note= '
620
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/note= '
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880
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/note=
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/note=
53.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
misc_feature
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AAD34214;
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0 0 0 0 0 0 0 0
                                                                        00000
                                                                                                                                                                                                                                                                                                                                                                                              Human cytochrome P
Human chemically p
Human immune syste
CDNA sequence #431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CYP2D6 gene,
Human CYP2D6 gene,
Human CYP2D6 gene,
                                                          20:43:59; Search time 16.6596 Seconds (without alignments) 5542.256 Million cell updates/sec
                                                                                                                                                                                                                                                                1. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3. /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
4. /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
5. /SIDS2/gcgdata/geneseqn-embl/NA1984.DAT:*
5. /SIDS2/gcgdata/geneseqn-embl/NA1984.DAT:*
6. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
7. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                              ctttgtgtgtgggtgattttct......crtgtgtaatcgtgtccctg
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       5.1.3
Compugen Ltd.
                                                                                                                                                                          Potal number of hits satisfying chosen parameters:
                                                                                                                                                         2185239 segs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
        GenCore version
Copyright (c) 1993 - 2003
                                                                                      US-09-942-310-2_COPY_920_960
                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
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ABQ72215
AAD34213
AAH26169
AAH26179
ABH39958
ABL32556
ABK36040
                                                                                                                               IDENTITY_NUC Gaport 1.0
                                                           February 10, 2003,
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                                                                                                                                                                                            seq length: 0
seq length: 200000000
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6472
6472
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2299
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Match
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40.6
40.6
40.2
40.2
31.6
331.6
                                                                                                                               Scoring table:
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                                                                                                      Perfect score:
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/note= "Known single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution V7M" replace (1031, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Known single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution VIIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single nucleotide polymorphism (SNP); as Y in the specification; causes the acid substitution P34S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= p
/label-PS12
/note= "Rovel single nucleotide polymorphism (SNP);
             single nucleotide polymorphism (SNP); as R in the specification" C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single nucleotide polymorphism (SNP); as K in the specification"
                                                                            "Novel single nucleotide polymorphism (SNP); given as Y in the specification" (769, C)
                                                                                                                                                                                                          Novel single nuclectide polymorphism (SNP); given as R in the specification" (825, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Novel single nucleotide polymorphism (SNP); given as S in the specification"
                                                                                                                                                    //note= "Novel single nucleotide polymorphism (SNP);
given as S in the specification"
replace (776, G)
                                                                                                                                                                                                                                                                                //note= "Known single nucleotide polymorphism (SNP);
given as R in the specification"
replace (915, C)
                                                                                                                                                                                                                                                                                                                                                Novel single nucleotide polymorphism (SNP); given as Y in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                   "CYP2D6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace (1019, A)
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/label= PS6
/note= "Novel s
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1884..2055
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                                     given
                                                                          /label= PS2
/note= "Novel
                         /note= "Novel
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                                                (678,
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/label= PS10
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/label= PS3
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/label= PS7
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             PS1
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/label= PS5
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0;
                                                                                                                                                                                                                                                                                                                                                          The invention relates to sequence determination oligonucleotides for abtencing polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase; antiarrhythmic; arrhythmia; adrenoreceptor antagonist; hypertension; tricyclic antidepressant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                 New sequence determination oligonucleotides, useful for detecting polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%; Score 40.6; DB 24; Length 1680; 100.0%; Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1680 BP; 413 A; 379 C; 539 G; 342 T; 7 other;
                                                                                                                                                                                                                      Oliasson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             920 CTTGTGTGGGTGATTTTCTGCRTGTGAATCGTGTCCCTG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCTG 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CYP2D6 gene, SEQ ID NO:1 version #1.
942
/*tag= f
/note= "Polymorphic site"
1255
                                                   /*tag= g
/note= "Polymorphic site"
                                                                                                                                                                                                                      Lewander T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO72215 standard; DNA; 6472 BP
                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 63pp; English.
                                                                                                                                           2001WO-IB01544.
                                                                                                                                                                   30-AUG-2000; 2000GB-0021286
                                                                                                                                                                                             (GEMI-) GEMINI GENOMICS PLC
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                                                                                         WO200218638-A2
 misc_feature
                                       misc_feature
                                                                                                                                           27-AUG-2001;
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ABQ72215
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Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme; chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenasc; antiarrhythmic; arrinythmia; adrenoreceptor antagonist; hypertension; tricyclic antidepressant; procainamide; drug induced lupus syndrome; environmentally linked disease; Parkinsons's disease; haplotyping; genotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Novel single nucleotide polymorphism (SNP);
given as R in the specification; together
with PS30 causes the amino acid substitution
V1361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                            /note: "Novel single nucleotide polymorphism (SNP); given as W in the specification; causes the amino acid substitution F1201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes "Novel single nucleotide polymorphism (SNP)" replace (678, C) /*tage b /label PS2
                                                                                                                                                                                                                                                                                                                                                    /notes "Novel single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution W128R"
                                                                                                                /ucce- "Novel single nucleotide polymorphism (SNP); given as S in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notem "Novel single nucleotide polymorphism (SNP)"
                                                            /note- "Known single nucleotide polymorphism (SNP); given as R in the specification" replace (2179, C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.6; DB 24; Length 6472;
Pred. No. 2.1e-06;
1; Mismatches 0; Indels 0;
given as Y in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CYP2D6 gene, SEQ ID NO:1 version #2.
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               (2170, A)
                                                                                                                                                                                                                replace (2611, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replace (2661, C)
                                                                                                                                                                                                                                                                                                                                                                                                   (2659, A)
                                                                                                                                                                                                                                                                                                         (2635, C)
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/label~ PS29
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larity 97.6%;
Conservative ]
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                                              /label- PS25
                                                                                                          /*tag: ae
/label- PS26
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/label⇔ PS27
                                                                                                                                                                                                                                                                                                                                       /label- PS28
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/number= 3
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les 40; Conserv
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Matches
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given as W in the specification; together
with PS18 causes the amino acid substitution
T107F."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /noter "Novel single nucleotide polymorphism (SNP); given as Y in the specification; together with PSI7 causes the amino acid substitution T107F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel single nucleotide polymorphism (SNP); given as R in the specification" (2067, G)
                                                                         /notes "Known single nucleotide polymorphism (SNP); given as M in the specification; causes the amino acid substitution L91M"
                                                                                                                                                                   Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution H94R"
                                                                                                                                                                                                                                                                                                                                     Novel single nucleotide polymorphism (SNP); given as Y in the specification; causes the amino acid substitution V104A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single nucleotide polymorphism (SNP); given as R in the specification; causes the amino acid substitution IlO9V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note "Known single nucleotide polymorphism (SNP);
given as Y in the specification"
2056..2605
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given as K in the specification"
replace (2118, T)
 given as R in the specification; causes the amino acid substitution R88H"
                                                                                                                                                                                                                                                            /note: "Novel single nucleotide polymorphism (SNP); given as S in the specification"
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given as Y in the specification"
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                                                                                                                                                                                                                                                                         given as (2014, C)
                              (1974, A)
                                                                                                                                                                                                                                                                                                                                                                                  (2022, T)
                                                                                                                        (1984, G)
                                                                                                                                                                                                                (1997, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2023, T)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (2036, C)
                                                                                                                                                                     /note- "Novel
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/label= PS13
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/label= PS14
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/label= PS21
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/label~ PS24
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/label~ PS23
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/number= 2
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/note= "Novel single nucleotide polymorphism (SNP);
causes the amino acid substitution V104A"
replace (2022, T)
                                                                                                                                          /note= "Novel single nucleotide polymorphism (SNP);
together with PS17 causes the amino acid
substitution T107F"
replace (2028, G)
                                                                                                                                                                                                                                                                                                            /*tag= y
/label= PS21
/note= "Known single nucleotide polymorphism (SNP)"
                                                                /note= "Novel single nucleotide polymorphism (SNP); together with PS18 causes the amino acid substitution T107F" replace (2023, T)
                                                                                                                                                                                                                     /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution I109v" replace (2036, C)
                                                                                                                                                                                                                                                            /*tag= x
/label= PS20
/note= "Novel single nucleotide polymorphism (SNP)"
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causes the amino acid substitution F1201"
replace (2635, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Novel single nucleotide polymorphism (SNP); together with PS30 causes the amino acid substitution V1361" replace (2661, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= ae
/labbl= ps26
/note= Novel single nucleotide polymorphism (SNP)"
2606..2758
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                                                                                                                                                                                                                                                                                                                                                                                     /cons_splice= (5'site:NO, 3'site:YES)
replace (2062, G)
                                                                                                                                                                                                                                                                                                replace (2039, T)
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                                                    /label= PS17
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/label= PS18
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/label= PS19
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/label= PS22
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/label= pS27
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/label= PS29
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/label= PS30
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/label- PS11
/note= "Known single nucleotide polymorphism (SNP)".
                                                                                                                                        /note= "Known single nucleotide polymorphism (SNP)", replace (915, C)
                               /note= "Novel single nucleotide polymorphism (SNP)" replace (776, G)
                                                                                      /note= "Novel single nucleotide polymorphism (SNP)"
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//label= ps6
houte= "Novel single nucleotide polymorphism (SNP)"
1001.5217
                                                                                                                                                                                                                                                                                                                                                          /*tag= j
/label= PS8
/note= "Known single nuclectide polymorphism (SNP);
causes the amino acid substitution VIIM"
replace (1100, T)
                                                                                                                                                                                                                                                                                                                     /note= "Known single nucleotide polymorphism (SNP);
causes the amino acid substitution V7M"
replace (1031, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Known single nucleotide polymorphism (SNP); causes the amino acid substitution P34S" 1181..1883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Novel single nucleotide polymorphism (SNP)" replace (1843, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution R88H"
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    causes the amino acid substitution L91M"
replace (1984, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Novel single nucleotide polymorphism (SNP)"
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/product= "CYP2D6"
1001..1180
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/*tag= i
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replace (1966, A)
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/*tag= t
/label= PS16
replace (769, C)
                                                                                                    replace (825, A)
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/*tag= m
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/label= PS10
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/label= PS13
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/label= PS12
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/label= PS15
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/label= PS4
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/label= PS5
                          /label= PS3
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/label= PS9
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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 205 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                       Score 40.6; DB 24; Length 9432; Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytochrome P450; CYP2D6; promoter; drug metabolism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "5' region of CYP2D6 coding region"
                                                                                                                                                                                           Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 other;
                                                                                                                                                                                                                                                      Indels
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'note≕ "amplification primer upr1669"
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/note~ "amplification primer upf14"
                                                                                                                                                                                                                                                                                  Human cytochrome P450 CYP2D6 gene promoter region.
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/note= "sequencing primer R3"
complement (968.988)
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'note= "sequencing primer F2"
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'note= "sequencing primer F3"
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/note= "sequencing primer R4"
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1650..1669
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                                                                                                                                                                                                                                                    1; Mismatches
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/note= "sequencing primer
complement (565..577)
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/note= "sequence primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (14..36)
                                                                                                                                                                                                                                                                                                                                                                                       AAH26169 standard; DNA; 1669
                                                                                                                                                                                                                       99.0%;
ilarity 97.6%;
Conservative
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Best Local Similarity
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                                                                                                                                                                CYP2D6 gene.
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                                                                                                                                                                                                                                                      Matches
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11gase-based sequenced determination; drug metabolism; chromosome 22;
"Known single nucleotide polymorphism (SNP); together with PS29 causes the amino acid substitution V1361"
                                                                                                                                                                                                                                                    /*tag- an
/label- PS33
/note- "Known single nucleotide polymorphism (SNP)"
                                                                                      /note "Known single nucleotide polymorphism (SNP); causes the amino acid substitution Q151E"
                                                                                                                                                              /note= "Novel single nucleotide polymorphism (SNP); causes the amino acid substitution E155K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New sequence determination oligonucleotides, useful for detecting bolymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in ligase-based sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%; Score 40.6; DB 24; Length 6472;
llarity 97.6%; Pred. No. 2.1e-06;
Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andersson MK, Lewander T, Oliasson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytochrome P450 2D6 (CYP2D6) gene.
                                                                                                                   replace (2716, A)
                                                                                                                                                                                                                                       (2846, A)
                                                                                                                                                                                                                                                                                                                                                                                       replace (3292, A)
                                            (2704, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Flg 1; 63pp; English
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                                                          /*tag= ak
/label= PS31
                                                                                                                                                /label- PS32
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/number= 4
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                                                                                                                                                                                          2759..2846
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                                                                                                                                                                                                                         /number-
                                            replace
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   /note-
                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-329785/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200218638-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Risinger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002
                                            variation
                                                                                                                                                                                                                                                                                                                                                                                      variation
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Human cytochrome P450 CYP2D6 gene promoter (G mutation at -1584 bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A polynucleotide capable of hybridizing to CYP2D6 promoter useful the optimization of drug therapies using substrates of cytochrome
                                         Cytochrome P450; CYP2D6; promoter; drug metabolism; diagnosis; therapy; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                             /frequency= "20%"
                                                                                                                                                                         replace(36,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-EP00954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000; 2000EP-0101889
                                                                                                                                                                                                                                                       /*tag= b
1620..1669
/*tag= c
                                                                                                                                                                                                                                                                                                                 /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raimundo S, Zanger U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-457734/49.
                                                                                                                                                                                                                                                                                                                                                                              WO200155432-A2.
                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                                                                                                      variation
                                                                                                                                                                                                                                 5'UTR
                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                   Key
  The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene. The promoter region was amplified CYPCDFORD Gene. The promoter region was amplified by CYPCDFORD Gene. The promoter region was amplified by PCR from leucocyte DNA of over 50 individuals, and sequenced. B Previously unknown single nucleotide polymorphisms (SNP) were identified. These were at: base 36 (base -1584 according to the CC G occurring at an estimated frequency of approximately 20% in the Whole population, and resulting in increased enzyme activity.

CC G, occurring at an estimated frequency of approximately 20% in the control position 386 (-1235), A to G, approximately 20% in the control position 386 (-1235), A to G, approximately 50% frequency, neutral function; position 620 (-1000), G to A, approximately 30% frequency, unknown function; position 940 (-680), C G to A, rare, unknown function; and 1298 (-322), T to C, rare, unknown function The C to G mutation at -1584 bp is strongly associated with lower metabolic ratios, and a molecular variant polymored and a thin increased acceptor-antagonist, tricyclic reduced or enhanced capacity for clearance of CYP2D6 substrates of antidepressant, selective scrotonin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or succeptibility to such a contact or enhanced capacity for clearance of a mutation at the CYP2D6 promoter. The strong association of the common C to G mutation at correlation between genotype and phenotype in the CYP2D6 polymorphism. Testing for the mutation will allow the identification of intermediate metabolism cannot the invival or any of me metabolism cannotype in the common contact on in viva drug metabolism cannotype in the cyp2d6 polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                           polynucleotide capable of hybridizing to CYP2D6 promoter useful for the optimization of drug therapies using substrates of cytochrome P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in vivo drug metabolism capacity, thus providing a very potent
of for improving the therapy of diseases with drugs that are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1669 BP; 413 A; 376 C; 534 G; 338 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTTGTGTGGGTGATTTTCTGCRTGTGAATCGTGTCCCTG 41
                                                                                                                                                                                 (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene product.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 41pp; English.
                                                                                                   30-JAN-2001; 2001WO-EP00954
                                                                                                                                          31-JAN-2000; 2000EP-0101889
                                                                                                                                                                                                                             Raimundo S, Zanger U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Best 39; Conserva
                                                                                                                                                                                                                                                                 WPI; 2001-457734/49.
                 WO200155432-A2.
                                                          02-AUG-2001
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/note= "5' region of CYP2D6 coding region"

Location/Qualifiers

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Gaps
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Note: The present sequence is not shown in the specification but is derived from the CYP2D6 promoter sequence given in the Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonist, tricyclic antidepressant, selective serotonin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP2D6 promoter. The novel variant forms of the CYP2D6 gene provided by the invention provide the potential for the development of a pharmacodynamic profile of drugs for a given patient. The finding and characterization of variations in the
                                                                  The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene, which includes G at position 36 base -1584 according to the Human Cytochrome P450 Allele Nomenclature). The presence of C at position -1584 bp is a marker for low enzyme activity, whereas there is strong association of at position -1584 bp with increased enzyme activity. The C to G single nucleotide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates (antiarrhythmic, beta-adrenergic receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 CTTTGTGTGGGGGATTTTCTRCGTGTGTAATCGTGTCCCTG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40.2; DB 22
Pred. No. 2.2e-06;
; Mismatches 0
Claim 1(a); Page -; 41pp; English.
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95.1%;
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Best Local Similarity
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AAH26179 standard; DNA; 1669 BP

RESULT 6 AAH26179

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(first entry)

17-SEP-2001 AAH26179;

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4302 TITGIGIGGGIGATITITIGIATGIGIAATCGIGITITIG 4341

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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDHG (NM_000693), CYP1A (NM_000781), CYP1B1 (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000191), CYP1B1 (NM_0001997), CCLN (NM_000380, TXNRD1 (NM_001999), UGT8 (NM_001989), CCLN (NM_001999), AND (NM_001990, NM_019902, NM_019902, NM_019909), NM_019903, NM_019902, NM_019903, NM_01
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                                                                                                                                                                                                                                                               Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP1181; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Now nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
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85.0%; Pred. No. 0.0077;
1.1ve 1; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5884 BP; 1259 A; 92 C; 1514 G; 3019 T; 0 other;
                                                                                                                                                                                                               Human chemically pretreated gene sequence #20 strand 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 39; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                               ABK39958 standard; DNA; 5884 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001; 2001WO-EP07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-154757/20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200202806-A2,
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                          21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2002
                                                                                                    ABK39958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek A,
RESULT 7
                            ABK39958
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antinflammatory; cancer disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia, Alzheimer's disease, AIDS, epilopsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.1%; Score 31.6; DB 24; Length 5884; 85.0%; Pred. No. 0.0077; 1.1ve 1; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5884 BP; 1259 A; 92 C; 1514 G; 3019 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 529; 32pp + Sequence Listing; German.
                                                                                                                                          Human immune system associated gene SEQ ID NO: 529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4302 TTTGTGTGGGTGATTTTTTGTATGTGTAATCGTGTTTTTG 4341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
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                                   ABL32556 standard; DNA; 5884
                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                       (first entry)
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                           WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002
                                                                    ABL32556;
                                                                                                                                                                                                                                                                                                      gene; ds.
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                ABL32556
RESULT
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Gaps

2 TTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41

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Matches 34; Conservative

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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the compares associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000491), CYP1B1 (NM_000497), CYP343 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_001979), CALN (NM_000776 and NM_017460), DPYD (NM_001980), CM_NM_001990, NM_019900, NM_019902, NM_019902, NM_01980, NM_01980), NM_019900, NM_019901, NM_019902, NM_01986, NM_01980, NM_019900, NM_019901, NM_019902, NM_01980, NM_01980, NM_01980, NM_01980, NM_01980, NM_01980, NM_01980, NM_019900, NM_019900, NM_01980, NM_01980,
      cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5884 BP; 1730 A; 92 C; 1381 G; 2681 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1584 CTTTATATATATATTTTCTACATATATAATCGTATCCCT 1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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72.58;
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                                                                                                                                                                                                                                                                          29-JUN-2001; 2001WO-EP07470.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-154757/20
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Matches 29; Conserv
                                                                                                                                                       WO200202806-A2
                                                                                                   Homo sapiens.
                                                                                                                                                                                                                  10-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
ABL32557/c
         QΥ
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                                                    Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avallie ER, Collins-Racie LA, Evans C;
Agostino MJ, Bowman MR, Spaulding V, Wong GG;
Howes SH, Resnick RJ, Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The CDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperboliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allegic conditions (e.g. asthma), neurodegenerative disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represent the CDNA sequences of the invention that encode for novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
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cDNA sequence #431 encoding novel human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 311-312; 393pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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72.5%;
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Best Local Similarity 72.5
Matches 29; Conservative
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Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCCOV JM,
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Clark HF,
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2000US-0198123.
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2000US-0209467.
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2000US-0225266.
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2000US-0232398.
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2000US-0190076
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2000US-0217496
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19-MAY-2000;
07-JUN-2000;
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30-JUN-2000;
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26-JUL-2000;
26-JUL-2000;
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22-AUG-2000;
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                                                               31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and neutlar degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AnDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirtheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
           antlarterlosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhoumatic; antiarthritic; antidabetic; antipsoriatic; antilnflammatory; cancer, disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Length 5884;
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                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 530; 32pp + Sequence Listing; German.
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ABA17450 standard; DNA; 6281 BP
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72.58;
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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(HUMA-) HUMAN GENOME SCI INC
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Barash SC, Ruben SM;

Rosen CA,

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(ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and outer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune than the adrenal gland, autoimmune therolitics and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. crebral anoxia and parasitic infections.
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                                      Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                  relates to novel genes (ABA11004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                           Disclosure; SEQ ID NO 9781; 1701pp + Sequence Listing; English.
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                                                         useful for preventing, cancers and metastases
WPI; 2001-541565/60.
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(HUMA-) HUMAN GENOME SCI INC

ŝ Ruben Barash SC, Rosen CA,

WPI; 2001-541565/60

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system useful for preventing, cancers and metastases

ID NO 9780; 1701pp + Sequence Listing; English. Disclosure; SEQ The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB4678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

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               marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
ovarian cancer and other cancers of the adrenal gland, bone, bone
                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                             Length 6286;
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The invention features to methods for predicting toxic effects by determining the compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the compound of these toxic defect, preferably the cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the effect of a compound or progression of a toxic effect, preferably the expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates to a computer toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, as the information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
                                                                                                                                                                                                                                                                      Rat sequence differentially expressed in response to a hepatotoxin #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods for predicting toxic effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elashoff MR;
                                                                                                                                                                                                                                                                                                               Rat; ss; hepatotoxin; expressed sequence tag; EST; drug sc:
differential expression; centrilobular necrosis; steatosis
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                     Db 100854 TITGIGIGITIGICIGIGIGIGIGIGIGIGI 100820
2 TITGIGIGGGTGATITICIGCRIGIGAATCGTGT
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                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-290029P.
2001US-290645P.
2001US-292336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-295798P.
2001US-297457P.
2001US-298884P.
                                                                                                                                            ABK62119 standard; cDNA; 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-2001; 2001WO-US23872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-222040P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-244880P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-2001; 2001US-303459P
                                                                                                                                                                                                                            18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-241625/29.
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22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-NOV-2000;
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                                                                                                     RESULT 15
                                                                                                                       ABK62119,
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Gaps

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Indels

7;

Score 23.4; DF Pred. No. 29; 1; Mismatches

57.18; 77.18;

Query Match Best Local Similarity

ä

27; Conservative

Matches

DB 23; Length 160755;

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CC toxicity markers in drug screening and toxicity assays. The genes and cC gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell cC sample that has been exposed to a compound or agent. Hepatotoxicity CC sample that has been exposed to a compound or agent. Hepatotoxicity c is characterised by centrilobular necrosis and steatosis. The present CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene CC which is differentially expressed in response to a hepatotoxic agent. XX

SQ Sequence 500 BP; 185 A; 115 C; 82 G; 121 T; 0 other;

Query Match

SG 18, Score 23; DB 24; Length 500;

Best Local Similarity 70.7%; Pred, No. 12; Mismatches 11; Indels 0; Gaps 0;
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Search completed: February 11, 2003, 02:06:10 Job time : 34.6596 secs

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Perfect score:

Sequence:

OM nucleic -

Run on:

Scoring table:

Minimum DB : Maximum DB :

Database

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

En (Dases 1 to 1180)

In (Dases 1 to 1180)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12828 row: d column: 07

High quality sequence start: 3

High quality sequence start: 3
                                                                                                                                                       A1758738 ty15e06.x
A1824445 tx70c11.x
R98298 yr30e08.r1
B38696 HS-1048-A2-
R49180 y958b09.s1
BM761459 K-EST0042
A1580308 tm40g04.x
A1880312 wn12a03.x
A1662312 ms08c10.x
                                                                                                                                                                                                                                        BH050434 RPCI 24-2
BE046391 hn46e03.x
BH063439 RPCI 24-3
BM842494 K-EST0119
AA456410 LM0206J24
AA56410 LW89908.x
BE85542 7914401.x
BE855473 7914401.x
BC554798 H4030D04-
BE857133 7919112.x
AZ342501 LM0075A10
AL015703 F. rubripe
AL015703 F. rubripe
AL131399 F. ubripe
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AGENCOURT_6643098 NIH_MGC_121 Homo sapiens cDNA clone iMAGE:5768406
BQ067695
                         F03457 HSC1YA062 n
N10553 yx86b06.r1
A1055032 ow75004.x
BE652228 275733 MA
BE623020 up32d04.y
B1999135 1031070H0
AL268930 TCLCaddon
BG918351 602819648
AA034947 ZK25604.s
BH274434 CH230-155
AA652245 ns69a03.s
                                                                                                                                       BF552720 UI-R-CO-1
AZ099911 RPCI-23-2
                  AA607596 vo07h12.r
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FR0043907
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B38696
R49180
BM761459
A1580308
A168312
BH050434
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BH063439
BH063439
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AZ426410
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BH274434
AA652245
AA483727
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AZ099911
AI758738
AI824445
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human.
                                                                        DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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BG657500 TGEST2ya2
BE371772 601217955
BF355613 602054008
BM14203 L0801B08-
AL284612 Tetraodon
                                                             ; Search time 118.283 Seconds (without alignments) 5613.764 Million cell updates/sec
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                                                                                                                   1 ctttgtgtgtgggtgattttct......crtgtgtgtaatcgtgtccctg
                                                                                                                                                                                    32308132
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                 16154066 segs, 8097743376 residues
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                US-09-942-310-2_COPY_920_960
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                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              sw model
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BG657500
BE371772
BF535613
BM114203
CNS04CLN
                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                             nucleic search, using
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                                                               February 10, 2003,
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length: 2000000000
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gb_htc:*
gb_est3:*
gb_est4:*
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Result . 9 ; 0

Gaps

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excised as phagemids and rescued in SOLR cells. The plasmid library was recovered from the SOLR cells and transformed in mass into DH10B (GeneHog, Research Genetics, Inc.) for sequencing. WARNING: This library may contain a small percentage contaminants from human fibroblast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE371772 618 bp mRNA linear EST 21-JUL-2000 601217955F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3587125 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH "MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM8749 row: m column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

169 c 151 g 117 t
lambda vector (Stratagene). The primary library was mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:3587125"
/clone_lib="NCI_CGAP_Lu29"
/fissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                               Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 618;
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                                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                    234 GTGTGGGTGGTTTCCTCCGTGTAAATGTGGCTCGCTG 270
                                                                                                                                                                                                                                                                                                                                         5 GTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCTG 41
                                                                                                                                                                                                                                                                   Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25.2; E
Pred. No. 54;
1; Mismatches
                                                                                                                                                                                                                                               Score 25.4;
Pred. No. 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C2ECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 6
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE371772.1 GI:9317135
                                                                                                                                                                                                                                            62.0%;
78.4%;
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75.0%;
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Best Local Similarity 75.0%
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.45
Matches 29; Conservative
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BE371772
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LOCUS
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                                                                                                             Abb_host="Organ: brain; Vector: pcMV-SPORT6; Site_1: Not1; Note="Organ: brain; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGESTZYAZOGO6.Y1 TGVEG118 Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TGESTZYA20g06.y1 5', mRNA sequence.
BG657500.1 GI:13797767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI : This library was constructed by Keliang Tang, Robert Cole, and L. David Sibley at Washington University. cDNAS were synthesized from poly(A)+ RNA by olidod(T) priming, size-selected and directionally cloned into the Uni-ZAP XR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: toxo@watson.wustl.edu
contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Cliffon, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.6; DB 14; Length 1180;
Pred. No. 0.00015;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="TgESTzya20g06.y1"
/clone_lib="TgVEG118 Tachyzoite cDNA Library"
/dev_stage-rachyzoite"
/deb_nost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Toxoplasma gondii"
                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5768406"
/clone_lib="N'H_MGC_121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: -40RP Irom classifiers tigh quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sarcocystidae; Toxoplasma.
1 (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="VEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.0%;
Best Local Similarity 97.6%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Clifton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                        254
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DEFINITION
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VERSION
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BG657500
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SOURCE
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COMMENT

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microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal3 (Ref. Development 127:1737-1749 (2000) [PMID:1072249]), purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were digested with Sal1 and NotI enzymes, and cloned into Sal1/NotI site of BSPORTI plasmid vector. The DH10B E. Col1 host was trashformed with ligation mixture by the standard chemical method. The average lisert size is about 1.9 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: brain; Vector: pSPORTI (Invitrogen); Site_1: Sali; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA). Intramural Research Program, NIH (http://lgsun.grc.nla.nlh.gov/cDNA). Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSO4CLN 915 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone 099D06 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS: genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis.

Tetraodon nigroviridis.

Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

I (bases 1 to 915)

Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.,

Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer [Invitrogen: 5'-pGACTGGCGGCCGCCTTTTTTTTTTTTTTTT-3'] from 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 915)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                            /db_xref="niaEST:L0801B08-3"
/db_xref="niaEST:L0801B08-3"
/db_xref="taxon:10090"
/clone="L0801B08"
/clone="Lib="NIA Mouse Newborn Brain cDNA Library"
/tissue_type="Newborn Brain"
/dev_stage="Newborn Brain"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                       quality sequence stop: 499
                                                                          Location/Qualifiers
  Seq primer: -21M13 Forward
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AL284612.1 GI:8023003
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Matches 31; Conserv
                                                  POLYA-Yes.
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                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xrefe"taxon:10090"
/clone="IRAGE:1193496"
/clone="IRAGE:1193496"
/lab host="DH108 (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAF Library."
1 307 c 325 g 156 t 1 others
                     BF535613 1055 bp mRNA linear EST 11-DEC-2000 602054008F1 NCI_CGAP_SG2 Mus musculus CDNA clone IMAGE:4193496 5', mRNA sequence.
BF535613. GI:11622981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 30-JAN-2002
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BM114203
BM114203.1 GI:17077221
EST.
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Plao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Lim, M.K. and Ko, M.S.H.
                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 1055)
IIH-MGC http://mgc.nci.nlh.gov/.
                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbbs-rémail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0801 row: B column: 08
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Contact: Dawood B. Dudekula
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9555 row: o column: 01
High quality sequence stop: 676.
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75.0%; Pred. No. 60;
iive 1; Mismatches 9;
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Matches 30; Conservative
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BF535613/c
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20-MAY-2001
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                                                                                                                                                                                                                                                                                                BG787054 1036 bp mRNA linear EST 20-MAY-2003
SEAUMC007011 Sea urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PM990802-02-0457 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 1036)
Zhu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. and
Ettensohn, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A large scale analysis of mRNAs expressed by primary mesenchyme cells of the sea urchin embryo Development 128 (13), 2615-2627 (2001)
                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucchinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; dt priming from poly A+ RNA, directionally cloned" 223 c 197 g 263 t 4 others
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/db_xref="taxon:7668"
/clone="PM990802-02-0457"
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/lab_host="E.coli"
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Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh, PA 15213, USA
TTel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
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77.8%;
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76.3%;
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Matches 28; Conservative
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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ (Lone=TiMAGE.405336"
/ (Lone=Lib="NIH_MGC_46"
/ (Lissue type="leiomyosarcoma cell line"
/ Lissue type="leiomyosarcoms cell line"
/ Lissue made by oligo-dT priming. Directionally cloned into constructed by Ling Hong in the laboratory cell derald M. Rubin (University of California, Berkeley)
using zAP-CDNA synthesis kit (Stratagene) and Superscript Library."
                                                       Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis penome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1. 915
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="1099006"
/clone_lib="6"
/clone_lib="6"
/note=""Genoscope sequence ID : COBG099DB03SPl-end :
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NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 31.
Location/Qualifiers
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Tissue Procurement: ATCC
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Best Local Similarity 72.2%;
Matches 26; Conservative
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                                                    Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 302)
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.C., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Poullot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                           Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6"
/db_xref="taxon:10090"
/clone="InAGE:1040807"
/clone=lib="Stratagene mouse skin (#937313)"
/sexo"females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.0%; Score 24.2; DB 9; Length 302; llarity 74.4%; Pred. No. 1.18+02; Conservative 1; Mismatches 9; Indels
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                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
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                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
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ENAMONO Sapiens

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tavaskis, E., Watcrston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washingert EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Sitc_1: HindIII;
/sitc_2: NotI; sex=Female: dev_stage: 3 months old;
/solate=muscular atrophy patient; tissue_type-total brain
/total mRNA was oligo-(dT) primed and directionally
cloned 5. > 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N36563 16-JAN-1990 yx86b06.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268595 5' similar to contains L1.t3 L1 repetitive element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
High quality sequence stops: 225
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1602 Std Error: 0.00
                                                                      Tel: 33169472800
Fax: 33160778698
Fax: 33160778698
Single read. removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_ldt: alc-lya06
Seq primer: (-21)M13_universal.
Location/Qualifiers
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                       Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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                                                                                                                                                                                                                                                                                                                                                                               /clone_lib~"normalized infant brain cDNA" /sex~"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TITGTGTGGGTGATTITCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.0%; Score 24.2; DB 14
llarity 72.5%; Pred. No. 1.1e+02;
Conservative 1; Mismatches 10
                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-1ya06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 225.
Location/Qualifiers
1.,353
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Seq primer: T7
Genexpress-Genethon
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Best Local Similarity
Matches 29; Conserv
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81

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109

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source
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ACCESSION
                                                                                                                                                                 RESULT 13
BF652228/c
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BASE COUNT
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BE623020/c
                                                                  Matches
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COMMENT
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KEYWORDS
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0
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Emall: Ggapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (inf@limage.llnl.gov) for further information.
Insert Length: 873 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                        Gaps
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/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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                                                                                                                                                                                                                                                                                          59.0%; Score 24.2; DB 14; Length 353; 72.5%; Pred. No. 1.1e+02; Live 1; Mismatches 10; Indels 0;
                                                    /clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                2 TTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/organism="Homo sapiens"
/db_xref="GDB:3878237"
                                       /clone="IMAGE:268595"
                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Matches 29; Conserv
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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                                                                                                                                                                                                                                                                ORIGIN
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoidea; Bovoinae; Bos.

1 (bases 1 to 506)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-NcKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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/lab_host="DHIOB"
//nab_worter: pcWv SPORT6; Site_1: Not1; Site_2: Sal1;
//note=worter: pcWv SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
llorgissimus muscle."
77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                  Gaps
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                                                                   Length 387;
                                                                                                                                                                                                                                                                                                                                 BF652228 506 bp mRNA linear 275733 MARC 3BOV Bos taurus CDNA 5', mRNA sequence. BF652228
                                                                                                                  Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4830
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
                                                                   Score 24.2; DB 9;
Pred. No. 1.1e+02;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 65 row. E column: 2
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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б
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PCR PRimers
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                                                                   59.0%;
74.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
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                                                                                                                  29; Conservative
                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
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source
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                                                                                                    FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."
BE623020 383 bp mRNA linear EST 24-AUG-2000 up32d04.yl Soares_mouse_NMGB_bcell Mus musculus cDNA clone IMAGE:2698663 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDernott, J.P., Shrager, J., Shiflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oliga(dr) primer (5'
rettaccaarcigaagregeagegececcregriffittititititititit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:2698663"
/clone=lib="Soares=mouse_NMGB_bcell"
/lab_bost="DH10B (phage-resistant)"
/note="Organ: germinal B-cell, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                 1 (bases 1 to 383)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 10;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%; Sco. 75.0%; Pred. No. 1... 0; Mismatches
                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40RP from Gibco
High quality sequence stop: 339.
Location/Qualifiers
1. .383
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Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
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                                                                                                BE623020.1 GI:9903426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:1034187
                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
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                                                                        ACCESSION
VERSION
                                                                                                                                                                  ORGANISM
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                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                               COMMENT
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Purham, NC 27708-1000

Tel: 919 613 8139

Fax: 919 613 8179

Fax: 919 613 8179

Email: chauserfauke.edu.

Email: clocation/Qualificrs

Location/Qualificrs

1. 4320/Qualificrs

Location/Qualificrs

Location/Cualificrs

1. 4320/Qualificrs

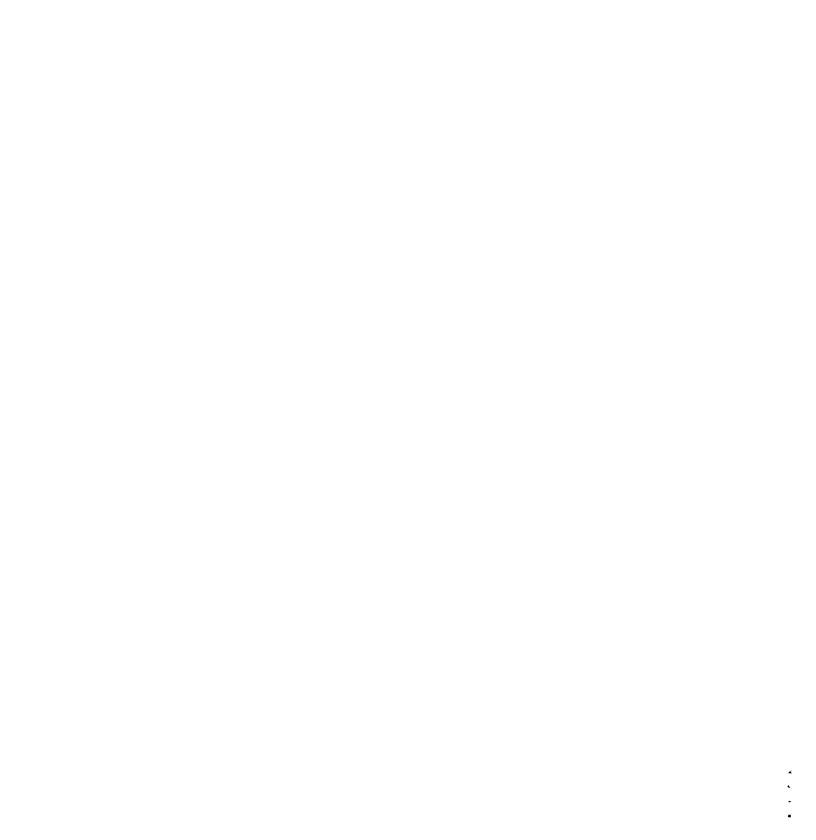
Location/Cualificrs

1. 4320/Qualificrs

Location/Cualificrs

Loc
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Search completed: February 11, 2003, 03:31:24 Job time: 123.283 secs



us-09-942-310-2_copy_920_960.rni

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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
4784
6350
6350
15144
38564
169998
600
600
17425
22067
246240
                                                                                                            61
439
2274
                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
STREET: 60 St.
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-253-155A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Sequence 3, Appli
Batent No. 5395760
Sequence 9, Appli
Sequence 11, Appl
Sequence 13, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 62, Appli
Sequence 46, Appli
Sequence 32, Appli
Sequence 32, Appli
Sequence 41, Appli
Sequence 81, Appli
Sequence 10, Appli
                                                 February 10, 2003, 21:12:29 ; Search time 3.11557 Seconds
(without alignments)
4035.781 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                            Sequence 4, Appl
                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                            1 ctttgtgtgggtgattttct......crtgtgtaatcgtgtccctg
                                                                                                                                                                                                               version 5.1.3 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-762-308-11
US-09-844-634-10
US-08-650-000-3
5395760-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-936-135-9
US-08-936-135-11
US-08-936-135-13
US-09-021-287-2
US-09-240-473-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-458-434A-4
                                                                                                                                 441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                       US-09-942-310-2_COPY_920_960
                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    nucleic search, using sw model
                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
       GenCore
Copyright (c) 1993
                                                                                                                                                              length: 0
length: 2000000000
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392
2169
10684
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Match
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Maximum DB
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Sequence 6, Appl 1
Sequence 3, Appl 1
Sequence 24, Appl 1
Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 5, Appl 1
Sequence 5, Appl 1
Sequence 20, Appl 1
Sequence 21, Appl 1
Sequence 22, Appl 1
Sequence 22, Appl 1
Sequence 22, Appl 1
Sequence 22, Appl 2
Sequence 22, Appl 3
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Womena, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
RARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
LENGTH: 50000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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US-08-936-135-15
US-08-385-335A-9
US-08-458-434A-6
US-09-734-673-3
US-09-734-673-3
US-09-75-041-5
US-09-67-66108-24
US-08-599-252-104
PCT-US96-06532-104
PCT-US96-06533-104
US-09-820-0011-3
US-09-820-0011-3
US-08-724-394A-21
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Patent No. 569147
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giullo
TITLE OF INVENTION: CDR4 Binding Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: LAHIVE & COCKFIELD 60 State Street
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71.18;
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Best Local Similarity 71.1.
Matches 27; Conservative
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6068976
                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-618-100B-3
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Patent No. 606
US-08-618-100B-3
                                                              US-08-806-326-5
  FEATURE
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Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Atweh, George F.
TITLE OF INVENTION: VECTORS FOR GENE THERAPY OF ERYTHROID
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FEACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/806,326
FILING DATE: 26-FEB-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/398,160
FILING DATE: 03-MAR-1995
ATONNEY/AGENT INFORMATION:
NAME: Clark Richard S.
REGISTRATION NUMBER: 26,154
REGISTRATION NUMBER: 26,154
REGISTRATION NUMBER: 26,154
REGISTRATION NUMBER: 26,154
TELECHONE: 212-408-2558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 CTTTGGGAGATTGGTTTTTTCCGTGGATTATCCTGCCCTG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
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                                                   CONTROL TAFFLLIALON JOURNELS: US/08/253,155A
ETLING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNDABER: MII-028
REFERENCE/DOCKET NUMBER: MII-028
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617) 227-7400
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08806326
Patent No. 6022738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.2%;
Best Local Similarity 68.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        LENGTH: 392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212-765-2519
                    ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: cDNA
US-08-253-155A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-806-326-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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Gaps
                                                                                                                                      0;
                                                                                     Length 2169;
                                                                                                                                        Indels
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DESCRIPTION: Sequence between exon 1 and exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Briggs, Michael R.
APPLICANT: Auwerx, Johan
APPLICANT: de Vos, Piet
APPLICANT: de Staels, Bart
APPLICANT: Croston, Glenn E.
APPLICANT: Miller, Stephen G.
TITLE OF INVENTION: MODULATORS OF OB GENE AND
TITLE OF INVENTION: SCREENING METHODS THEREFOR NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,100B
FILING DATE: March 19, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/558,588
FILING DATE: APPLICATION NUMBER: 08/510,584
FILING DATE: APPLICATION NUMBER: 08/510,584
FILING DATE: APPLICATION NUMBER: 08/418,096
FILING DATE: APPLICATION NUMBER: 08/418,096
FILING DATE: APPLICATION NUMBER: 08/418,096
APPLICATION NUMBER: 08/418,096
FILING DATE: MARCH 20, 1995
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            1 CTTTGTGTGGTGATTTTCTGCRTGTGTAATCGTGT 36
                                                                                     ; Score 21.2; DE; Pred. No. 15; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219/075
                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08618100B Patent No. 6068976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
                                                                                       Query Match 51.7%;
Best Local Similarity 72.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEPRAX: (213) 955-0440
TELES: 67-3510
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 10684 base pairs
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 90071-2066
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                     STATE:
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 Score 21; DB 3; Length 10684;
Pred. No. 25;
1; Mismatches 11; Indels (
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Tischer, Itzhak
APPLICANT: Tischer, Itzhak
APPLICANT: Inwinton: Limbic System-Associated Membrane
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SOUGHNESS: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                   .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                             2 TTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1078 TGTGTGTGTGTGTGTGTGTGTGTGTAATAGTG 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.8; DE Pred. No. 21; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TITGTGTGGGTGATTTTCTGCRTGTGTAATCGTG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317743-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/414,657D FILING DATE: 31-MAR-1995 CLASSIFICATION: 435 CLASSIFICATION A35 APPLICATION NUMBER:
                                                                                                                                                                                                              Sequence 20, Application US/08414657D Patent No. 5861283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09135080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.78;
73.58;
 51.2%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence
LOCATION: 877...1032
CTHER INFORMATION:
US-08-414-657D-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
Query Match
Best Local Similarity 69.2 Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.7
Best Local Similarity 73.5
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 609-520-32
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 08543
COMPUTER READABLE FORM:
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                                                                                                                                                                                            US-08-414-657D-20
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US-09-135-080-5
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STATE:
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GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHÖLIPASE A2, GROUP VI (CA2+-INDEP
FILE REFERENCE: RTS-0220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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APPLICANT: Levitt, Pat R.
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISCHRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
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CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 70000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/09851896
; Patent No. 6410325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 609-620-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 877...1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.7%;
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 609-620-3259
                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                           Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 877...1
; OTHER INFORMATION:
US-09-135-080-5
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GENERAL INFORMATION:
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                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DGWILT Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
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                                                                                                                               Gaps
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                                                                                  Score 20.6; DB 4; Length 70000;
Pred. No. 51;
1; Mismatches 10; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 0597 171914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.4; DB 1;
Pred. No. 15;
1; Mismatches 12;
                                                                                                                                                                                       DD 55508 GTGTTTGCATGTGTGCATGTGTGCGTGTCCATG 55472
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                                                                                                                                                                 5 GIGIGGGIGATITICIGCRIGIGAAICGIGICCCIG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09865.601
                                                                                                                                                                                                                                                                                       Sequence 62, Application US/08222177A Patent No. 5582979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-222-177A-46/c; Sequence 46, Application US/08222177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION: (608) 831-2100
TELEFRAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                        50.2%;
70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 67.5%;
Matches 27; Conservative 1
                                                                                        Query Match
Best Local Similarity 70.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; IMMEDIATE SOURCE:
; CLONE: mfd4rs
US-08-222-177A-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                    ; FEATURE:
US-09-851-896-3
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APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type= "tandem"
/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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OTHER INFORMALL.
OTHER INFORMALL.
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: 126..145
LOCATION: 126..140
THEORYMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name="PCR primer"
TNFORMATION: /citation= [[1]]
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NAME/KEY: misc_feature
LOCATION: complement (215..236)
LDEWTIFCOATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                    ZIP: 3317-1914

COMPUTER READABLE FORM:
MEDUUM TYPE: Floppy disk
COMPUTER: DEPENDED FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RALEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence= EXPERIMENTAL
                                                                                                                 ADDRESSEE: DeWitt Ross & Stevens, S.C. STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..262
IDENTIFICATION METHOD: experimental
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: repeat_region LOCATION: 172..205 OTHER INFORMATION: /rpt_t OTHER INFORMATION: /rpt_t OTHER INFORMATION: /citat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: Mfd84
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Ca
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                                                                                                                                                            Madison
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                                                                                                                                                                                                             USA
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Gaps
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                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08486924
Patent No. 5789197
GENERAL INFORMATION:
APPLICANT: Wetterau II, John R.
APPLICANT: Sharp, Daru Y.
APPLICANT: Gregg, Richard E.
TITLE OF INVENTION: MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
NUMBER OF SEQUENCES: 32
CORRESPONDENCES. 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
                                                                                           Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,924
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
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                                                                                      Query Match 49.8%; Score 20.4; DB 1; Best Local Similarity 67.5%; Pred. No. 24; Matches 27; Conservative 1; Mismatches 12;
                                                                                                                                                                         2 TITGIGIGIGIGATITICICCRIGIGIAAICGIGICCCIG 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPICATION: 45.7

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,362
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
REFERNCE/COCKET NUMBER: 33,111
REFERNCE/COCKET NUMBER: 32.11
FELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-5901
TELEPHONE: (609) 252-5901
TELEPHONE: COOP, 252-5901
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 439, Application US/09641638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.5%;
Matches 27; Conservative
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          repeat_region
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US-09-641-638-439/c
                                                                                                                                                                                                                                                                          RESULT 11
US-08-486-924-32/c
        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-486-924-32
                            ; LOCATION:
US-08-117-362-32
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GENERAL INFORMATION:
APPLICANT: Wetterau II, John R.
TITLE OF INVENTION:
TITLE OF INVENTION: MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STRIE: New Ierro.
      /standard_name= "Only one strand sequenced"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.4; DB 1; Length 262;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                           PUBLICATION INFORMATION:
AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Abundant Class of Human DNA Polymorphisms
TITLE: Which Can Be Typed Using the Polymerase Chain
TITLE: Reaction
OTHER INFORMATION: /standard_name= "Only one stra
PUBLICCATION INFORMATION:
AUTHORS: Webter, J. L.
AUTHORS: Kwitek, A. E.
AUTHORS: May, P. E.
TITLE: Dinuclectide repeat polymorphism at the
TITLE: Dissa locus
JOURNAL: Nucleic Acids Res.
VOLUME: 18
PAGES: 4637-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,362
FILING DATE: 03-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 TGTGTGTGTGTGTGTGTGTGTGTGTGTCCGTGTATCTG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-117-362-32/c
; Sequence 32, Application US/08117362
; Patent No. 5595872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (609) 252-5901
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Am. J. Hum. Genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.5%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey COUNTRY: U.S.A. ZIP: 08543-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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PAGES:
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COUNTRY: USA
ZIP: 2006-1888
COMPUTER READABLE FORM:
MEDUIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MURSHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.8%;
67.5%;
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.53
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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SOFTWARE: Patentin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-599-252-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-436-074-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                              APPLICANT: BOUGUELECT, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENSET.051CP1
FILE REFERENCE: GENSET.051CP1
CURRENT APPLICANTON NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
SEGURDANE: PARCH FILING DATE: 1999-03-12
SEGURDANE: PARCH FILING DATE: PARCH FILIN
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LOCATION: 502.521
OTHER INFORMATION: 12-776-259.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 243..263
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 674..692
OTHER INFORMATION: downstream amplification primer
COTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
49.8%; Score 20.4; DB 4; Length 900;
Best Local Similarity 67.5%; Pred. No. 26;
Matches 27; Conservative 1; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-776-259 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD TO DIAGNOSE HEREDITARY HEMOCHROMATOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 rererererererererererererererererere 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-776-259 potential probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 12-776-259.misl, potential
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Patent No. 5705343
GENERAL INFORMATION:
APPLICANT: PEDER, JOHN N.
APPLICANT: REDER, JOHN N.
APPLICANT: THOMEL, ANDREAS
APPLICANT: THOMEL, BRUCE E.
APPLICANT: THOMES, WINSTON J.
APPLICANT: ROLER, R.
APPLICANT: WOLFF, ROGER F.
TITLE OF INVENTION: METHOD DIAGN
TITLE OF INVENTION: HEMOCHROMATOSIS
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-641-638-439
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US-08-599-252-81
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LENGTH: 900
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Patent No. 5755438

GENERAL INFORMATION

APPLICANT: PEDER, JOHN N.

APPLICANT: FEDER, ANDREAS

APPLICANT: KIMMEL, BRUCE E.

APPLICANT: KIMMEL, BRUCE E.

APPLICANT: MOLEF, ROGE E.

APPLICANT: MOLEF, ROGE E.

TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY

TITLE OF INVENTION: HEMOCHROMATOSIS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,252
FILING DATE: 09-FFB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: MORRISON & FOERSTER
: 2000 Pennsylvania Ave. N.W., Suite 5500
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: US/08/436,074
FILLING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TITGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20.4; DE Pred. No. 27; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                    TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 887-1500
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Pred. No. 27;
1; Mismatches 12; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 81, Application PC/TUS9606352
GENERAL INFORMATION:
APPLICANT: DAYNA, DENNIS T.
APPLICANT: EEDER, JOHN N.
APPLICANT: FEDER, JOHN N.
APPLICANT: HAMEL, BRUCE E.
APPLICANT: HAMEL, BRUCE E.
APPLICANT: HOMES, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 124
CORRESPONDENCES: 124
CORRESPONDENCES: 12000 Pennsylvania Ave. N.W., Suite 5500
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STRATE: DC
CONTRY: USA
ZOUG-1888
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06352
FILING DATE: BOPFEMATION:
APPLICATION NUMBER: US 08/599,252
FILING DATE: COPPEMATION:
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECHMINICATION NUMBER: 29,959
REFERENCE/COCKET NUMBER: 29,959
REFERENCE/COCKET NUMBER: 20,959
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 67.5%;
Matches 27; Conservative 1
                                                                                                                                                                                                                                 ; TOPOLOGY: 11near
US-08-436-074-54
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PCT-US96-06352-81
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PCT-US96-06352-81
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521 TGTGTGTGTGTGTGTGTGTGTGTAATAGAGGCTTTG 560
                                                                           Search completed: February 11, 2003, 06:00:20 Job time: 15.1156 secs
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Appl

Sequence 232, App Sequence 31, App 11 Sequence 11, App 11 Sequence 20, App 11 Sequence 20, App 12 Sequence 20, App 13 Sequence 1109, Ap Sequence 1107, Ap Sequence 1107, Ap Sequence 220, App Sequence 320, App Se

Sequence Sequence

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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APPLICANT: Castle, Arthur APPLICANT: Castle, Arthur APPLICANT: Castle, Arthur APPLICANT: Castle, Michael APPLICANT: Castle, Inchael APPLICANT: Castle, Inc. True of Invervior: Molecular Toxicology Modeling File Reference: 44921-538-US CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31 PRIOR FILING DATE: 2000-07-31 PRIOR FILING DATE: 2000-07-31 PRIOR FILING DATE: 2001-05-11 PRIOR APPLICATION NUMBER: US 60/290,645 PRIOR FILING DATE: 2001-05-11 PRIOR PRILOR DATE: 2001-05-15 PRIOR FILING DATE: 2001-05-16 PRIOR FILING DATE: 2001-06-06 PRIOR FILING DATE: 2001-06-06 PRIOR FILING DATE: 2001-06-19 PRIOR PRIOR FILING DATE: 2001-06-19 PRIOR PRIOR
                                                        US-10-099-841-99

US-09-962-832-332

US-09-991-653-13

US-09-991-053-11

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US-09-771-208-20

US-09-771-208-20

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US-10-190-593-3

US-10-1
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US-09-864-761-18793
US-09-864-761-3024
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US-09-864-761-9954
US-09-917-800A-881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09917800A Patent No. US20020119462A1 GENERAL INFORMATION:
   APPLICANT: Mendrick, Donne
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory

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Sequence 26, Applisequence 1162, Applisequence 1162, Applisequence 30, Applisequence 309, Applisequence 1297, Applisequence 1146, Applisequence 16, Applisequence 16, Applisequence 5, Applisequence 5, Applisequence 20, Appliseque
                                                                                                                                                                                                         February 11, 2003, 03:31:30 ; Search time 3.72137 Seconds (without alignments) 5222.300 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PUSNW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/DS06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-764-847-1161
0 US-09-764-846-303
0 US-09-764-846-309
0 US-09-864-761-12977
0 US-09-818-112-3
0 US-09-818-1146
0 US-09-744-761-1146
0 US-09-764-847-166
US-09-799-462A-16
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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8894
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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA799812 US-09-917-800A-26

ORGANISM: Rattus norvegicus

FEATURE

Sequence 2276, Ap Sequence 3478, Ap Sequence 3950, Ap Sequence 7571, Ap

US-09-954-456-2276 US-09-880-107-3478 US-09-867-701-7571 US-09-796-692-3950

220 221 221 221 221 221 221 231 24 24 24 25 27 27 27

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Result

US-09-796-692-3999

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TYPE: DNA
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LENGTH: 20
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1162
LENGTH: 5629
                                                                                                                                                                                              Sequence 7. Application US/10079623
Patent No. US20020169302A1
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: mammary gland and methods for their use.
FILE REFERENCE: 11000.104443
 Score 23; DB 10; Length 500;
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 366;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                        Indels
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                                                                                               324 CTCTGTGTGTGTGTCTGTGTGTGTGTTTTTTATATGCCTG 284
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                                        1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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Query Match 56.1%;
Best Local Similarity 70.7%;
Matches 29; Conservative
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Best Local Similarity 70.03
Matches 28; Conservative
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; ORGANISM: Homo sapiens
US-09-764-847-1162
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Best Local Similarity
Matches 28; Conserv
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; ORGANISM: Bovine
US-10-079-623-7
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US-09-764-847-1162
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US-09-764-847-1161
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US-10-079-623-7
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ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 309
LENGTH: 5591
                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 10; Length 6265;
Pred. No. 29;
GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Yan, Chunhua
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLOOL199
CURRENT APPLICATION NUMBER: US/09/820,905
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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; Patent No. US20020102638A1
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; OTHER INFORMATION: n = A,T,C or
US-09-820-905-3
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70.08;
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Best Local Similarity 70.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.09
Matches 28; Conservative
                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-764-847-1161
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                                                                                                                                                                                                                                              LENGTH: 6265
                                                                                                                                                                                                                       SEQ ID NO 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-820-905-3
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Gaps

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Indels

10;

Length 539,

DB 10;

26;

SIGNAL 0.56

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US-09-864-761-1146/c

Sequence 1146 Application US/09864761

Sequence 1146 Application Sharron G.

APPLICANT: Reark, David K.

APPLICANT: Ghen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: UNMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PRILING DATE: 2000-06-04

PRIOR PRILING DATE: 2000-06-03

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PRILING DATE: 2000-01-03

PRIOR PRILING DATE: 2000-01-03

PRIOR PRILING DATE: 2000-01-03

PRIOR PRILING DATE: 2000-09-27

PRIOR PRILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL \hookleftarrow 0.61 US-09-864-761-12977
                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 52.7%; Score 21.6; I Similarity 80.0%; Pred. No. 69; 24; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 23438 CTTTGTATGCCTCATTTTCTTCATGTGTAA 23467
                                                                                                                                Score 21.6;
Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NGS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 116592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)...(116592)
OTHER INFORMATION: n ~ A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09818512 Patent No. US20020142416A1
                                                                                                                            Query Match
Best Local Similarity 71.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-818-512-3
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                          ö
                                                                                                                                                             Gaps
                                                                                                                                                          0
                                                                                               Length 5591;
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OTHER INFORMATION: MAP TO ACO10634.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN PLACEMYA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
                                                                                                                                                          Indels
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 12977
LENGTH: 539
                                                                                            DB 10;
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                                                                                     Score 21.8; DE Pred. No. 34; 1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-09-37

PRIOR PRILING DATE: 2000-09-37

PRIOR PRILING DATE: 2000-09-37

PRIOR FILING DATE: 2000-09-37

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 09/608, 408

PRIOR APPLICATION NUMBER: US 09/714, 203

PRIOR APPLICATION NUMBER: US 09/714, 203

PRIOR APPLICATION NUMBER: US 09/714, 203
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12977, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                        Query Match 53.2%;
Best Local Similarity 74.3%;
Matches 26; Conservative
; ORGANISM: Homo sapiens
US-09-764-846-309
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ORGANISM: Homo sapiens
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Gaps

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Indels

Length 116592;

DB 10; ς .

Gaps

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Indels

12;

Mismatches

Conservative

28;

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Matches
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APPLICANT: Rosen et al.
TITLE OF INVENTION:
NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D IN PLACENTA, SIGNAL = 23
D IN BT474, SIGNAL = 11
D IN BONE MARROW, SIGNAL = 11
D IN LUNG, SIGNAL = 25
D IN HBLIO0, SIGNAL = 25
D IN BRAIN, SIGNAL = 28
D IN BRAIN, SIGNAL = 28
D IN BRAIN, SIGNAL = 28
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                    PRIOR APPLICATION UNMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00662
PRIOR PLICATION NUMBER: PCT/USO1/00662
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PLICATION NUMBER: US 09/608,408
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPRESSED IN FETAL LIVER, SIGNAL = EXPRESSED IN HELA, SIGNAL = 18 EXPRESSED IN ADULT LIVER, SIGNAL =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CICTGRGTGRGTGRGTGRGTGRGTGRGTGTGTGTCTG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.2%; Score 21.4; DB 10; 68.3%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Patent No. US20020132767A1
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Matches 28; Conservative
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US-09-764-847-1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
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US-09-764-847-1606
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Length 8894;

Score 21.4; DB 10; Pred. No. 52;

52.2%; 68.3%;

Query Match Best Local Similarity

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Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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CORRESPONDENCE HOLDERS: ADDRESSE: Holler Ehrman White & McAulliffe
STREET: 4250 Executive Square, 7th Floor
                        1 CTTTGTGTGTGTGTTTTCTGCRTGTGTAATCGTGTCCTG 41
1 CITIGIGIGIGATITICIGCRIGIGIAAICGIGICCCIG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,462A
FILING DATE: 10-Sep-2001
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                            Sequence 16, Application US/09799462A Patent No. US20020160970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%;
ilarity 68.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                    CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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Best Local Similarity
Matches 28; Conserv
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TYPE: DNA ORGANISM: Mus musculus
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Matches 28; Conserv
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US-09-771-208-20/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 659158
                                                                                                                                                                                                                               US-09-815-981-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 20
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                    δλ
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Sequence 16, Application US/10125767
Patent No. US20020160410A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                         FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                              ADDRESSEE: Heller Ehrman White & McAuliffe LLP STREET: 4350 La Jolla Village Drive, 7th Floor CITY: San Diego STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTTGTGTGGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.2%; Score 21.4; DB 9; Best Local Similarity 68.3%; Pred. No. 61; Matches 28; Conservative 1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
APPLICATION DATA:
APPLICATION NUMBER: 09/10/125,767
FILING DATE: 17-Apr-2002
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-ANG-1996
APPLICATION NUMBER: 08/695,191
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/692,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
APPLICATION NUMBER: 08/629,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanle L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402J
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-10-125-767-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 22118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09815981
Publication No. US20030003435Al
GENERAL INFORMATION:
APPLICANT: de Jong, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11near
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
                                                                                                                                                            NUMBER OF SEQUENCES: 34
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                USA
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Gaps
APPLICANT: Vandebyl, Sandra
TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID
TITLEOF INVENTION: MOLECULES INTO CELLS AND ASSESSMENT THEREOF
FILE REFERENCE: 24601-416
CURRENT APPLICATION NUMBER: US/09/815,981
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 22118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 22118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 20136 CTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGGGTG 20176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT, SUMON
TITLE OF INVERTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 12001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR FILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTTTGTGTGGGTGATTTTCTGCRTGTGAATCGTGTCCCTG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 61;
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LOCATION: (602485)
LOCATION: (602466).(602485)
NAME/KEY: misc_feature
LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified a, c, of the resolution of the re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΰ
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LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (183872)..(183891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (346860)..(346823)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09771208
Patent No. US200220155564A1
GENERAL INFORMATION:
APPLICANT: MEDRANO, JUAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.2%; Scilarity 68.3%; Pr
Conservative 1;
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GENERAL INFORMATION:

APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sects
FILE REPRENCE: 689290-76
CURRENT FILING DATE: 2001-09-18
FRIOR PELICATION NUMBER: US/60/233,617
PRIOR PELICATION NUMBER: US/60/233,617
PRIOR PELICATION NUMBER: US/60/234,923
PRIOR PELICATION NUMBER: US/60/234,923
PRIOR PELICATION NUMBER: US/60/235,334
PRIOR PELICATION NUMBER: US/60/235,637
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,720
PRIOR PELICATION NUMBER: US/60/235,840
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR PELING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                     Score 21.4; DB 9; Length 659158;
Pred. No. 1.1e+02;
1; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 73308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 447357 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGTGCCATG 447317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                               1 CTTTGTGTGGTGATTTTCTGCRTGTGTAATCGTGTCCCTG 41
; OTHER INFORMATION: n is unidentified a, c, g, or; NAME/KEY: misc_feature; LOCATION: (170655)..(170645); OTHER INFORMATION: n is unidentified a, c, g, or; NAME/KEY: misc_feature; LOCATION: (132680)..(132700); OTHER INFORMATION: n is unidentified a, c, g, or; NAME/KEY: misc_feature; NAME/KEY: misc_feature; oTHER INFORMATION: n is a, c, g, or t; US-09-771-208-20
             or
                                                                                                                                                                       or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.2; DB Pred. No. 90; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 11, 2003, 09:12:20 Job time : 113.721 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2276, Application US/09954456 Patent No. US20020115057A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.7%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
SEQ ID NO 2276
LENGTH: 73308
                                                                                                                                                                                                                                                                                                     Query Match 52.2%;
Best Local Similarity 68.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.7
Best Local Similarity 72.2
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2276
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US-09-954-456-2276
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60.09
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Human cytochrome P
Human cytochrome P
Human cytochrome P
Human foetal liver
Probe #1903 for g
Human brain expres
                                                                                                                                                       February 10, 2003, 20:43:59; Search time 16.6596 Seconds (without alignments) 5542.256 Million cell updates/sec
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1. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1980 DAT:*

2. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1981. DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1981. DAT:*

3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1982. DAT:*

5. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1985. DAT:*

7. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1985. DAT:*

7. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1985. DAT:*

8. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1980. DAT:*

9. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1980. DAT:*

110. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1980. DAT:*

121. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

132. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

143. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

154. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

155. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

166. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

177. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

188. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

189. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

180. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

181. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

182. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

183. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

184. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

215. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

216. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

217. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

218. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

229. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

231. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

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231. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

241. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

252. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

262. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT:*

273. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990. DAT
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                      5.1.3
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                     2185239 seqs, 1125999159 residues
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                        GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                   US-09-942-310-2_COPY_600_640
41
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Listing first 45 summaries
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AAH26179
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ABA40537
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Gapop 10.0 , Gapext 1.0
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Probe #25316 used Human genome-derly Human foetal liver Probe #308 for ge Human bone marrow Probe #12449 used Probe #12449 used Human polynucleoti Human genome-derly Human neall cycle a Human polynucleoti Human neall cycle a Human polynucleoti Human polynucleoti Human polynucleoti Human polynucleoti Human chosophila melanog Genomic sequence # DNA encoding propi Mycobacterium tube Mycobacterium tube Human breast cell Human horeast cell Human foetal liver Probe #1319 for g Probe #1319 for g Probe #1319 for g Human balan expres Human balan expres Human bone marrow Human bone marrow	human;
AA156630 ABS24124 ABA330842 AAR330842 AAK12168 AAK12168 AAA118650 AAI18650 AAI18650 AAI18650518 AAI18650518 AAI60518 AAI60518 AAI60614 AAI	ALIGNMENTS 1669 BP. P2D6 gene promoter region. promoter; drug metabolism; (ualifiers) tt (1436) mplification primer upf14" sequence primer R1" sequencing primer R2" tt (565577) sequencing primer R2" sequencing primer R2" tt (565577) sequencing primer R2" tt (565577) sequencing primer R2" tt (568988)
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	d; DNA;] rst entry P450 CYI P450 CYP2D6; Py; ds. COMPLEME A1313.358 A1313.358 A1313.358 A1493.314 A1493.
11111111111111111111111111111111111111	1 14126169; 7-SEP-20 1-SEP-20 14126169; 7-SEP-20 14200515 142005 14200515 142005 14200515 142
0 00 0 00 0 0 0 0	RESULT AAAASCELT AAAAASCELT AAAAAASCELT AAAAASCELT AAAAAASCELT AAAAASCELT AAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAASCELT AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

bone marrow #17595 for

Probe

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Sequence 1669 BP; 413 A; 376 C; 534 G; 338 T; 8 other;
f
"sequencing primer F3"
                                                                                                                (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                           cargets of the CYP2D6 gene product.
                                                                                                                                                            Claim 1; Fig 1; 41pp; English.
                                                                                                        31-JAN-2000; 2000EP-0101889
                                                                                               30-JAN-2001; 2001WO-EP00954
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1620..1669
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                      ..1623
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                                                                                                                         Raimundo S, Zanger U;
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                                                                              WO200155432-A2.
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                      primer_bind
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                                                5'UTR
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(EPID-) EPIDAUROS BIOTECHNOLOGIE AG
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Query Match
Best Local Similarity
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AAH26179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene. The promoter region was amplified by FOR from leucocyte DNA of over 50 individuals, and sequenced.

By PCR from leucocyte DNA of over 50 individuals, and sequenced.

By Previously unknown single nucleotide polymorphisms (SNP) were identified. These were at: base 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature), where the SNP was C to G occurring at an estimated frequency of approximately 20% in the population, and resulting in increased enzyme activity.

CC G occurring at an estimated frequency of approximately 20% frequency, neutral function; position 620 (-1000), G to A, approximately 20% frequency, neutral function; position 620 (-1000), G to A, approximately 30% frequency, unknown function; Dosition 940 (-680), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, approximately 30% frequency, unknown function; 1255 (-365), C G to A, rare, unknown function; and 1298 (-322), T to C, rare, c associated with lower metabolic ratios, and a molecular variant complexed with lower metabolic ratios, and a molecular variant complexed with intereased capacity for clearance of Cyp2D6 substrates of antidepressant, selective serotonin reuptake inhibitor, neutroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the Cyp2D6 promoter. The strong association of the common C to G mutation at C1884 bp with increased enzyme activity significantly improves the metabolisers and therefore allow menaholisers and therefore allow menaholisers and therefore allow menaholisers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A polynucleotide capable of hybridizing to CYP2D6 promoter useful for the optimization of drug therapies using substrates of cytochrome P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolizers and therefore allow quantitative predictions to be made on in vivo drug metabolism capacity, thus providing a very potent tool for improving the therapy of diseases with drugs that are
                                                                                                                                                                                                                                                                                                                                           'note= "5' region of CYP2D6 coding region"
                                                                                                                                                                                                            note= "amplification primer upr1669"
                                                           *tag= g
note= "sequencing primer R4"
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note= "sequencing primer R5"
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytochrome P450 CYP2D6 gene promoter (G mutation at -1584 bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antagonist, tricyclic antidepressant, selective servicin reuptake inhibitor, neuroleptic, opiate, cytostatic or amphetamine), or susceptibility to such a disorder, by determining the presence of a mutation in the CYP2D6 promoter. The novel variant forms of the GVP2D6 gene provided by the invention provide the potential for the development of a pharmacodynamic profile of drugs for a given patient. The finding and characterization of variations in the CYP2D6 gene, and diagnostic tests for the discrimination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the promoter region of the human cytochrome P450 CYP2D6 gene, which includes G at position 36 (base -1584 according to the Human Cytochrome P450 Allele Nomenclature). The presence of C at position -1584 bp is a marker for low enzyme activity, whereas there is strong association of G at position -1584 bp with increased enzyme activity. The C to G single nucleotide polymorphism occurs in approximately 20% of the population. The invention provides a method of diagnosing a disorder related to reduced or enhanced capacity for clearance of CYP2D6 substrates (antiarrhythmic, beta adrenergic receptor
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         Length 1669;
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                                                                                                Indels
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                                                                                                                                                                                                                       600 AGAAAGCAGTGGAGGAGGACRACCTCAGGCAGCCGGGAG 640
                                                                                                                                                                         1 AGAAAGCAGTGGAGGACRACCCTCAGGCAGCCCGGGAG 41
99.0%; Score 40.6; DB 22;
100.0%; Pred. No. 6.4e-05;
ive 0; Mismatches 0;
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polymorphic sites in a 5' flanking region of a CYP2D6 gene, as hybridization probes, as components of diagnostic assays, or in
                                                                                                          ligase-based sequence determination
                                                                                                                                   Claim 1; Fig 2; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic; ligase-based sequenced determination; drug metabolism; chromosome 22;
                                                                                                                                                                                                                                                    Gaps
                                                                          different alleles in human individuals, provide a very potent tool for improving the therapy of diseases with drugs that are targets of the CYP2D6 gene production, and whose metabolism is therefore dependent on CYP2D6 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                  he present sequence is not shown in the specification but from the CYP2D6 promoter sequence given in the Sequence
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                                                                                                                                                                                                                      Length 1669;
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                                                                                                                                                                                         535 G; 338 T; 7 other;
                                                                                                                                                                                                                                                                                          ; DB 22;
6.4e-05;
hes 0;
                                                                                                                                                                                                                                                                             1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
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99.0%; Score 40.6; D
Best Local Similarity 100.0%; Pred. No. 6.4
Matches 41; Conservative 0; Mismatches
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20 10:12:55 2003
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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic ability to metabolise certain drugs. The present sequence is human CYP2D6 gene 5' flanking region containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5° fianking region of cytochrome P450 2D6 (CYP2D5) gene. CYP2D6 enzymes are involved in the metabolism of fiany different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, sprobes in sequence determination methods based on mismatches, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenoblotic; ligase-based sequenced determination; drug metabolism; chromosome 22;
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                     Sequence 1680 BP; 413 A; 379 C; 539 G; 342 T; 7 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                              600 AGAAAGCAGTGGAGGACGACRACCTCAGGCAGCCGGGAG 640
                                                                                                                                                                                                                                                                                                                 , DB 24;
6.4e-05;
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                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 6.4
                                                                                                                                                                                                                                                                                                                 Score 40.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytochrome P450 2D6 (CYP2D6) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewander T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligase-based sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 1; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 9432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2001; 2001WO-IB01544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000GB-0021286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMI-) GEMINI GENOMICS PLC.
                                                                                                                                                                                                                                                                                                                 99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Risinger C, Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-329785/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD34213 standard;
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New sequence determination oligonucleotides, useful for detecting

Oliasson

Lewander T,

Andersson MK,

Risinger C,

WPI; 2002-329785/36

(GEMI-) GEMINI GENOMICS PLC. 30-AUG-2000; 2000GB-0021286 27-AUG-2001; 2001WO-IB01544

A CONTRACTOR OF A CONTRACT OF

49 AGAAGCCCCTGCTGGAGGACGACCTCAGGGTGCCAGGAAG 89

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WO200157274-A2
                                                                                                                                                                                                                                                                                         26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                               03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                   23-JAN-2002
                                                                                                                                                                                                                                    09-AUG-2001
                                                                             ABA40537;
                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                          Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK24652
                                             ABA40537
                                 RESULT
                                                                   δy
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0
                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \operatorname{Human} genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver \cdot
                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                             Length 9432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 24279; 639pp + sequence listing; English.
                                                       Sequence 9432 BP; 1964 A; 2647 C; 2976 G; 1845 T; 0 other;
                                                                                                   Indels
                                                                                                                                                                                                                                                                    Human foetal liver single exon nucleic acid probe #24279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid
                                                                                                                                    600 AGAAAGCAGTGGAGGAGGACGACCCTCAGGCAGCCGGGAG 640
                                                                        99.0%; Score 40.6; DB 24;
ilarity 97.6%; Pred. No. 7.2e-05;
Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.6; DB 22;
Pred. No. 19;
1; Mismatches 10;
                                                                                                                         1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 159 BP; 38 A; 50 C; 51 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-023686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.0%;
Best Local Similarity 73.2%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000GB-0024263.
                                                                                                                                                                                                  ABA75974 standard; DNA; 159
                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483447/52
                                                                                      Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                    WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2000;
04-OCT-2000;
                                   gene.
                                                                                                                                                                                                                                              01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                        ABA75974;
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                              RESULT 5
                                                                                                                                             qq
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                   Probe #19003 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                            Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 159 BP; 38 A; 50 C; 51 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID No 19003; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK24652 standard; DNA; 159 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%;
73.2%;
ABA40537 standard; DNA; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000GB-0024263
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK24652
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AGAAAGCAGTGGAGGACRACCTCAGGCAGCCCGGGAG 41

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WO200157278-A2
                                                      03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human;
          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #17595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                               30-JUN-2000;
                            04-FEB-2000;
                                      26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                           AAI27662;
                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe;
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                       The
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                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilopsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                             Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO: 24643; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed single exon probe SEQ ID NO: 25206.
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 159;
                         Human brain expressed single exon probe SEQ ID NO: 24643.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 159 BP; 38 A; 50 C; 51 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24.6;
Pred. No. 19;
                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed exon;
microarray; cancer; leukaemia; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-053366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.0%;
Best Local Similarity 73.2%;
Matches 30; Conservative
                                                                                                                                       2001WO-US00667
                                                                                                                                                                                                              2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK50649 standard; DNA; 159
        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                   Hanzel DK,
                                                               epilepsy; cancer; ss
                                                                                                                                                                                                                                                                   WPI; 2001-48346/52
                                                                                                  WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157276-A2
                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                      30-JAN-2001;
                                                                                 Homo sapiens
                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
        05-NOV-2001
                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                        nvention.
                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK50649;
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 159 BP; 38 A; 50 C; 51 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                            analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24.6;
Pred. No. 19
                                                                                                                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR;
                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-023659.
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                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI27662 standard; DNA; 159
                                                                                                                                                                                 2000GB-0024263
2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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20 T; 0 other;

51 G;

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for antenatal diagnosis of human genetic disorders.
                              Sequence 159 BP; 38 A; 50 C;
                                                                                                                                                                                                                                                                   ABS24124;
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                            Matches
                                                                                                                                                         49
                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                       ABS24124
                                                                                                                           QΥ
                                                                                                                                                       g
                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful
                                                                                                                                                                                                                       printed
                                                                                                                        (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                           present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #25316 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                  DB 22; Length 159;
                                               analyzing gene expression in human cervical epithelial cells
                                single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                             1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 159 BP; 38 A; 50 C; 51 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No 25316; 654pp; English.
                                                                              Claim 25; SEQ ID No 17595; 487pp; English.
                                                                                                                                                                                                                                                                                                                Score 24.6;
Pred. No. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                  60.0%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI56630 standard; DNA; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.29
Matches 30; Conservative
                                  qenome-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53
 WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI56630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                              The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid probes for measuring gene expression in a sample derived them human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; prinary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon probe ORF from lung SEQ ID No 24115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis;
                                                                   0;
   Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                       Indels
                                                                                                                                                                         AGAAGCCCCTGCTGGAGGACGACCTCAGGGTGCCAGGAAG 89
                                                                                                                                    1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                10;
DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measure gene expression in human lung samples
60.0%; Score 24.6; D
73.2%; Pred. No. 19;
cive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID No 24115; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                 ABS24124 standard; DNA; 159 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-180312P.
2000US-207456P.
2000US-0608408.
2000US-063366.
2000US-234687P.
2000US-2346359P.
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                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
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                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
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                                                                   30;
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA30842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA30842
            à
                                                                                                                                                                                                                                                                                                                                                                                                                  g
cc the cukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exors from genomic sequence by the method above und (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes of some as should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung disease.

CCOPD), interstitual lung disease (ILD), familial idiopathic pulmonary disease, such an analysis, pulmonary pulsatory sclerosis, Gaucher's disease, CC pulmonary alveolar proteinosis, Karagener syndrome, sarcoidosis, pulmonary alveolar proteinosis, Karagener syndrome, ilibrocystic pulmonary alveolar proteinosis, Karagener syndrome, sarcoidosis, pulmonary alveolar proteinosis, Karagener syndrome, ilibrocystic pulmonary alveolar proteinosis, Karagener syndrome, sarcoidosis, pulmonary data for this patent did not form part of the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic for the present sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24.6; DB 24;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 159 BP; 38 A; 50 C; 51 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA63649 standard; DNA; 555 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%;
73.2%;
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2000US-0234687,
2000US-0236359.
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2000US-0608408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
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21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA63649
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measuring human gene expression in a sample derived from human heart. The
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                                                   measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human hearts - \,
                                                                                                                                                                   printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #9308 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                              DB 22; Length 555;
Claim 1; SEQ ID NO 11954; 639pp + sequence listing; English.
                                        probe
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                         BP; 128 A; 158 C; 148 G; 121 T; 0 other;
                                      invention relates to a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                          298 AGAAGCCCCTGCTGCACGACCCTCAGGGTGCCAGGAAG 338
                                                                                                                                                                                                                                                                                                                                     1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCGGGAG 41
                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                             Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                            Score 24.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 9308; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                           Local Similarity 73.2%;
les 30; Conservative
                                                                                                                                                                                                                                                              60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA30842 standard; DNA; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157274-A2
                                                                                                                                                                                                                           Sequence 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001.
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Search completed: February 11, 2003, 02:05:41 Job time : 20.6596 secs
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monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 12159; 650pp + Sequence Listing; English.
                                                                                                                                   DB 22; Length 555;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe SEQ ID NO: 12159.
                                                                                                   Sequence 555 BP; 128 A; 158 C; 148 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 555 BP; 128 A; 158 C; 148 G; 121 T; 0 other;
                                                                                                                                                                                                      298 AGAAGCCCTGCTGGAGGACGACCTTCAGGGTGCCAGGAAG 338
                                                                                                                                                                                     1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                               10;
                                                                                                                                Score 24.6; DB Pred. No. 21; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                               1;
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73.2%;
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                           AAK12168 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss.
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                                                                                                                                              Local Similarity
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                Query Match
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Gaps

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Llarity 73.2%; Conservative

Query Match Best Local Similarity Matches 30; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                              Human bone marrow expressed single exon probe SEQ ID NO: 12445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO: 12445; 658pp + Sequence Listing; English.
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              298 AGAAGCCCTGCTGGAGGACGACCTTCAGGGTGCCAGGAAG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 AGAAGCCCTGCTGGAGGACGACCTCAGGGTGCCAGGAAG 338
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1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG
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Pred. No. 21
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26-MAY-2000, 2000US-0207456.
30-JUN-2000, 2000US-0608408.
03-AUG-2000, 2000US-0632366.
21-SEP-2000, 2000US-0236597.
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73.28;
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                                                                                                                                                    (first entry)
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                                                                                             AAK37888 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
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BM040921 603614630
BM792240 K-EST0072
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BM248080 60201776
BM728944 UI-E-E01-
BM702091 UI-E-C01-
BM702091 AGENCOURT
BM792091 AGENCOURT
BM7939658 602459726
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AM7927751 AM7976916
AM7927751 AM797751
AM7927751 AM797751
AM7927751 AM797751
AM792777145 AGENCOURT
AM79277714652 AM797777144
AM802995 ILZ-UM007
     AA351643 EST59477
A1276126 q170b05.x
B1033426 PM1-NN120
BM697806 UI-E-DX0-
BM674533 UI-E-EJO-
                                         AI963082 WL27a05.X
BQ575427 UI-H-E21-
                                                                                                                                                                                                                                                                                                                              BI910844 16-OCT-200 BRO BD MRNA linear EST 16-OCT-200 603068871F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217977 5',
                                                              BM792240
BG222601
AW964936
BF345885
BF448000
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BQ400812
BQ74652
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BG396658
RQ219839
AV927751
AMS60193
AZ832717
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BE346825
BE346227
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BI910844
BI910844.1 GI:16174292
                                                 113
117
110
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                                                                                   Homo sapiens
human.
VERSION
KEYWORDS
SOURCE
ORGANISM
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BI910844/c
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DEFINITION
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
AA126901 2116602.s
BM796175 K-EST0078
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BF755875 CM3-CT057
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BQ067695 AGENCOURT
                                             February 10, 2003, 20:51:09; Search time 118.283 Seconds (without alignments) 5613.764 Million cell updates/sec
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                                                                                           1 agaaagcagtggaggaggac.....accctcaggcagcccgggag
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Compugen Ltd
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       GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
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AA126901
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EST 16-OCT-2001

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DENKATYCE, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 265)

Hiller, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Legy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                   EST 14-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTGGAAGATTCGCGGCCGCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                           AA126901 265 bp mRNA linear EST 14-MAY-1
zl16e02.sl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:502106 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 869 Std Error: 0.00
Seq primer: -40Ml3 fwd. from Amersham
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                               Length 1180;
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/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
/dev_stage="adult"
                                                                                                                                    Indels
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Pred. No. 0.19;
       دډ
                                                                                                                                  1; Mismatches
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       208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 133.
Location/Qualifiers
     347 g
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                                                                               83.4%;
87.8%;
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     371 c
                                                                                                                                    36; Conservative
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Fax: 314 286 1810
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Best Local Similarity
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/iab_host="noling" |
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55 a 244 c 224 g 163 t
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Site_2: Ecorv (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dr primed and directionally cloned (Ecorv site is destroyed upon cloning). Average insert size 1.7 kb, insert size range full:-insert size and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LLAM12828 row: d column: 07
High quality sequence stop: 536.
High quality sequence stop: 536.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40.6; DB 13; Length 886;
Pred. No. 0.0012;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 AGAAAGCAGTGGAGGAGGACGACCTCAGGCAGCCCGGGAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
1. .886
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
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BQ067695
BQ067695.1 GI:19896741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.0%;
Best Local Similarity 97.6%;
Matches 40; Conservative
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BQ067695
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1. 366
/organism-"Homo sapiens"
/db_xefor"texon:9606"
/clone_lib="CT0570"
/dev_stage-"Adult"
/note="Organ: colon; Vector: puc18; Site_l: Smal; Site_2: Smal; Amin-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl::CM3&t2.:CM3-CT0570-050201-716-all&t30-2001-02-05&t40-1)

Seq primer: puc 18 forward

High quality sequence stop: 352.
1 (bases 1 to 366)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.K.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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1 (bases I to 379)
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
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Pred. No. 2.3e+02;
1; Mismatches 10;
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BF755875.1 GI:12103775
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Best Local Similarity 73.2%;
Matches 30; Conservative
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                                 AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 334)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                             BM796175 334 bp mRNA linear EST 05-MAR-2002 R-EST0078828 S22SNU16nl Homo sapiens cDNA clone S22SNU16nl-55-A04
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CM3_CT0570-050201-716-all CT0570 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note:"Organ: Stomach; Vector: pT7T3-Pac; Site_1: ECORI; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from ascitic fluids of Korean patients by Park J.G. et al. 1099, Cancer Res 50: 2773-2780."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.3e+02;
1; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Korea Research Institute of Bioscience & Biotechnology 52 Booun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
Fax: +82-42-860-4409
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/cell_line="SNU-16"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organismc"Homo sapiens"
/db_xrefc"taxon:9606"
/clone="$22$NU16n1-55-A04"
/sexc"F"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yongsung@mail.kribb.re.kr
Plate: 55 row: A column: 04
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High quality sequence stop: 334.
Location/Qualifiers
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BG954027.1 GI:14372198
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Best Local Similarity 73.2%;
Matches 30; Conservative :
                                                                                                                                                                             5', mRNA sequence.
BM796175
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/clone_lib="CT0570"
/clone_lib="CT0570"
/clone_lib="CT0570"
/clone_lib="CT0570"
/note="Organ: colon: Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 from ORESTES PCR (U.S. Letters Patent application No. 196 into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-CT0570-
301000-432-h08&t3=2000-10-30&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 13
High quality sequence stop: 379.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 381)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Fax: +55-11-2707001
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-CI0570-050201-716-h08&t3=2001-02-05&t4=1)
                                                        Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 2.4e+02;
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ilarity 73.28;
Conservative
                                                                                                                                                                                                                                         Tel: +55-11-2704922
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 402)

8 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,

O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Farle-Hughes, J., Fine, L.D., Fitzgerald

Cline, T.R., Cotton, M.D., Farle-Hughes, J., Fine, L.D., Fitzgerald

Cline, T.R., Cotton, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.W.,

Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D.P., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Hw, W.,

Hu,J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

Weter, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

Verter, J.C.
                                                                                                                                                                                                                                           /dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
//note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
//note_1: Info the profe (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
//note puc 18 vector: Reverse transcription of tissue
//note conditions."
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EST29477 Infant brain Homo sapiens CDNA 5' end, mRNA sequence.
AA351643. GI:2003983
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Nature 377 (6547 Suppl), 3-174 (1995)
96026280
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                                                                                                          1. .383
/organism="Homo sapiens"
Seq primer: puc 18 forward
High quality sequence stop: 383.
                                                                                                                                                                              /db_xref="taxon:9606"
/clone_lib="CT0570"
                                                                    Location/Qualifiers
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Bioinformatics
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73.2%;
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Fax: +55-11-2707001
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ORGANISM
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BM697806
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/db_xref="taxon:9606"  
/clone="inact=1877649"  
/clone="inact=1877649"  
/clone="inact=1877649"  
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/tissue_type="Pooled human melanocyte, fetal heart, and prequant uterus"  
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/lab_host="bridge liberation"  
/lab_host="bridge liberation"  
/site_1: Row RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NHHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-3489479. and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI276126 448 bp mRNA linear EST 29-JAN-1999
q170b05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877649
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1. .402
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/db_xrefe="taxon:9606"
/clone_lib="infant brain"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 448)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoetmage.llnl.gov) for further information. Insert Length: 1079 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 24.6; DB 9; Length 402;
llarity 73.2%; Pred. No. 2.4e+02;
Conservative 1; Mismatches 10; Indels
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Pred. No. 2.5e+02;
1; Mismatches 10;
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A1276126
A1276126.1 GI:3898400
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Best Local Similarity 73.2%;
Matches 30; Conservative
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les 30; Conserv
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             source
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SOURCE
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AI276126
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10.464
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/dw_stage="Adult"
/orde="crage="Adult"
Site_2: Smal; A mini-library was made by cloning products site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Eutrleostoml;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 464)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliuveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl:PMIst2:PMI-NNI207-15020-023-a01st3-2001-02-15st4-1)
Seq priner: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 464.
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UI-E-DXO-ago-a-04-0-UI.rl UI-E-DXO Homo sapiens cDNA clone
UI-E-DXO-ago-a-04-0-UI 5', mRNA sequence.
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      EST 14-JUN-2001
mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 2.5e+02;
1; Mismatches 10; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
BIO33426
MEN. NN1207-150201-023-a01 NN1207 Homo sapiens CDNA,
BIO33426.1 GI:14440052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           low stringency conditions.
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llarity 73.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
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VERSION

1 AGAAAGCAGTGGAGGAGGACRACCCTCAGGCAGCCCGGGAG 41

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ORGANISM

KEYWORDS

AUTHORS TITLE

REFERENCE

MEDLINE COMMENT

JOURNAL

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University of Ioward Town Indiana Ioward City, IA 52242, USA 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8250
Email: msoarcesblue weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adev_stage="fetal and adult"

Alab_host="HH10B (Life Technologies) (Tl phage resistant)"

Anote="Organ: eye; Vector: pr73-Pace (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I; and cloned directionally into pT773-pac vector. The oligonucleotide used to prime the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAGA, eye anterior segment, AATGCGGAT; optic nerve, CGATTAGGGA, eye anterior segment, AATGCGGAT; optic nerve, CGATTAGGGA, etclina, CGGCS, Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALYGAUB2 536 bp mRNA linear EST 09-MAR-2000 Wt27a05.xl NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2508656 3' similar to TR:070210 070210 CHONDROADHERIN. ;, mRNA sequence. A1963082
       1 (bases 1 to 506)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 24.6; DB 14; Length 506; 73.2%; Pred. No. 2.5e+02; Live 1; Mismatches 10; Indels 0
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                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
97044477
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                                                                                                                                                                                                                               Contact: Soares, MB
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Matches 30;
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AI963082
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KEYWORDS
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/dev_stage="fetal"
/dev_stage=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: MI3 Reverse.
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                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       1 (bases 1 to 470)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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Pred. No. 2.5e+02;
1; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-E-DX0-ago-a-04-0-UI"
/clone_lib="UI-E-DX0"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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Best Local Similarity 73.2%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                      97044477
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human.
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BASE COUNT

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Query Match
Best Local Similarity
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                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Esmect-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1465 Std Error: 0.00
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ575427 540 bp mRNA linear EST 19-JUN-2002 UI-H-EZI-bbb-b-02-0-UI.sl NCI_CGAP_Ch2 Homo sapiens cDNA clone UI-H-EZI-bbb-b-02-0-UI 3', mRNA sequence.
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Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 536)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                    NCI CGAP http://www.ncbl.nlm.nlh.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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BQ575427.1 GI:21478744
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Unpublished (1997)
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                                                                                      AUTHORS
TITLE
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Location/Qualifiers
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